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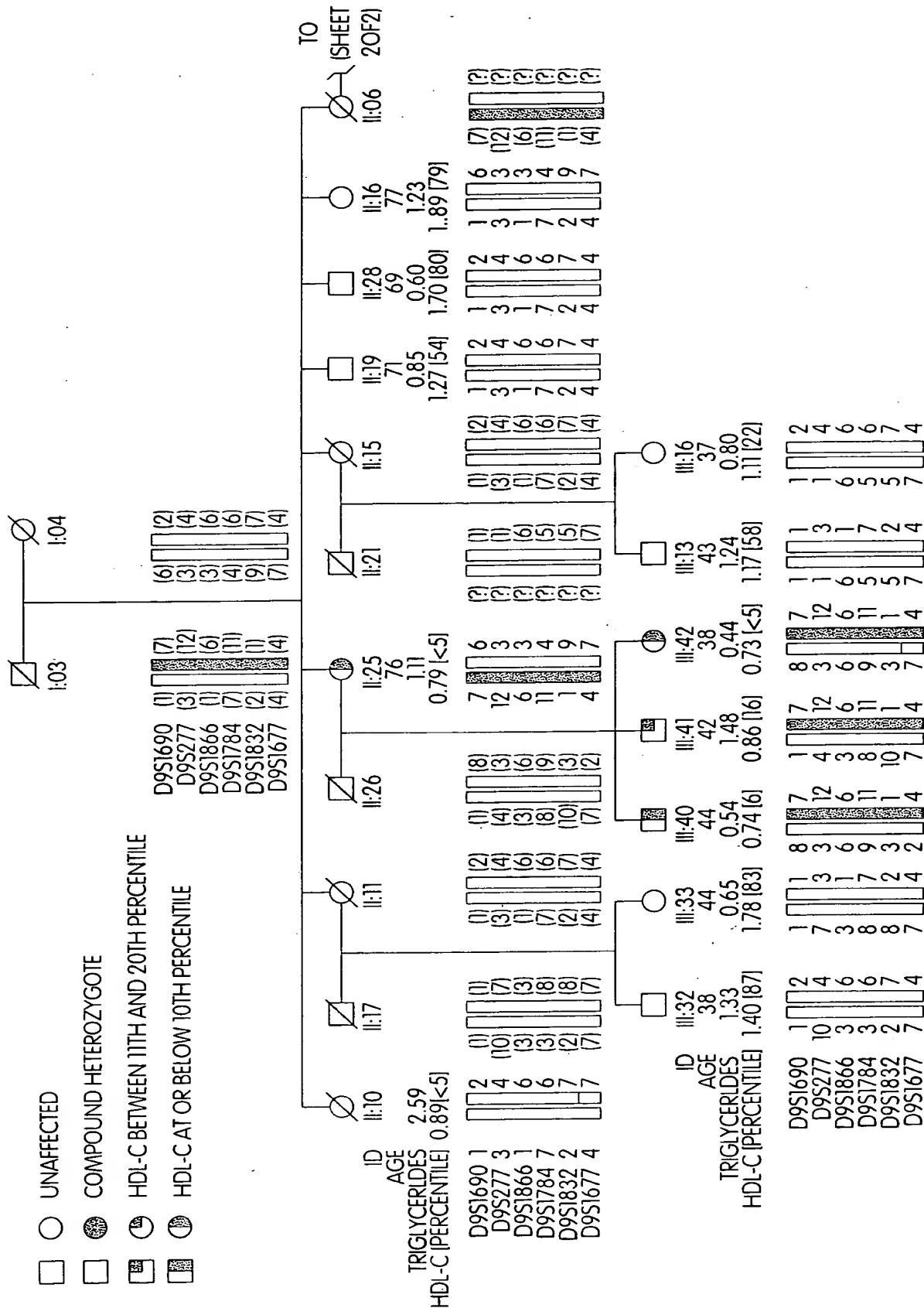


Fig. 1 (SHEET 1 OF 2)

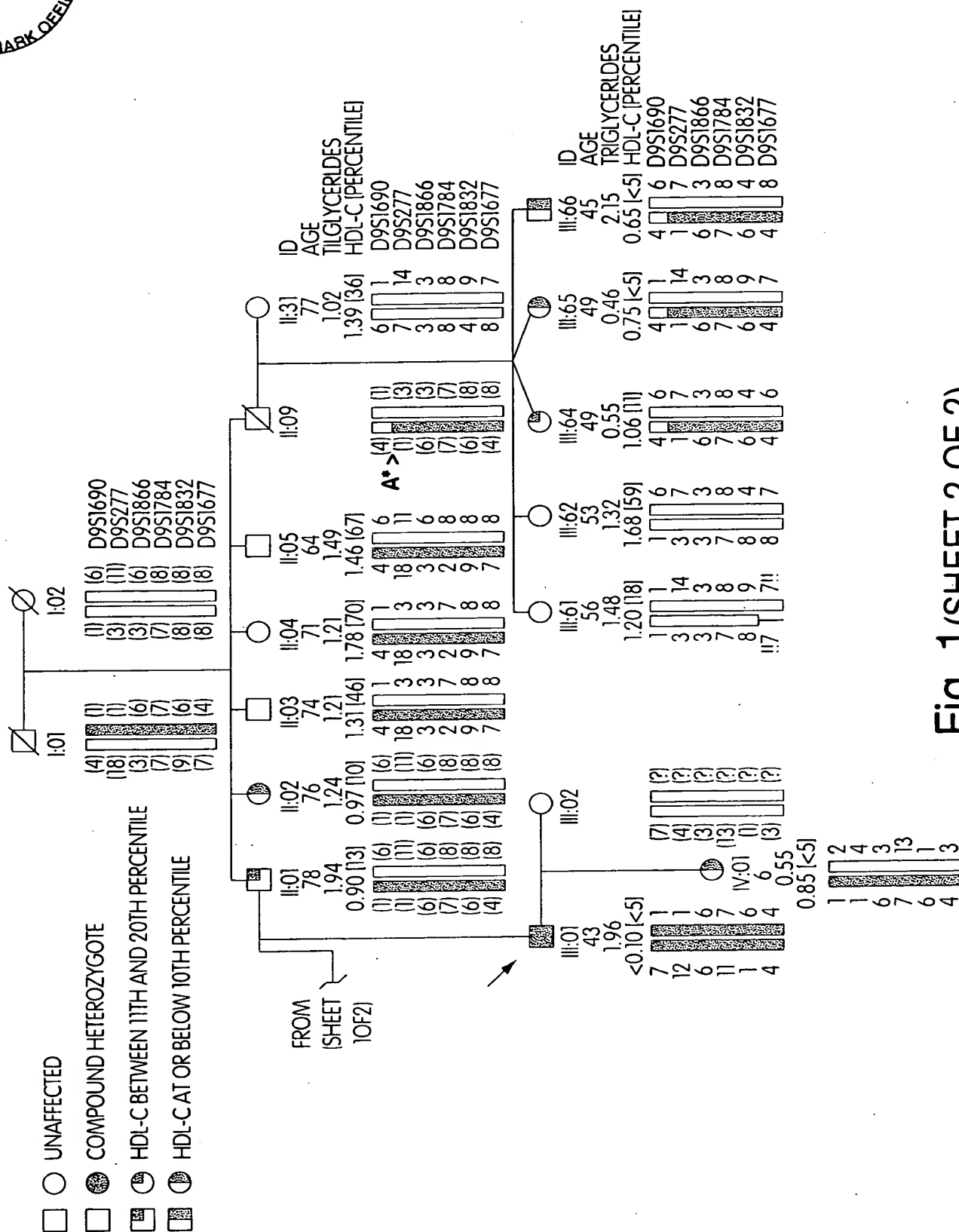


Fig. 1 (SHEET 2 OF 2)

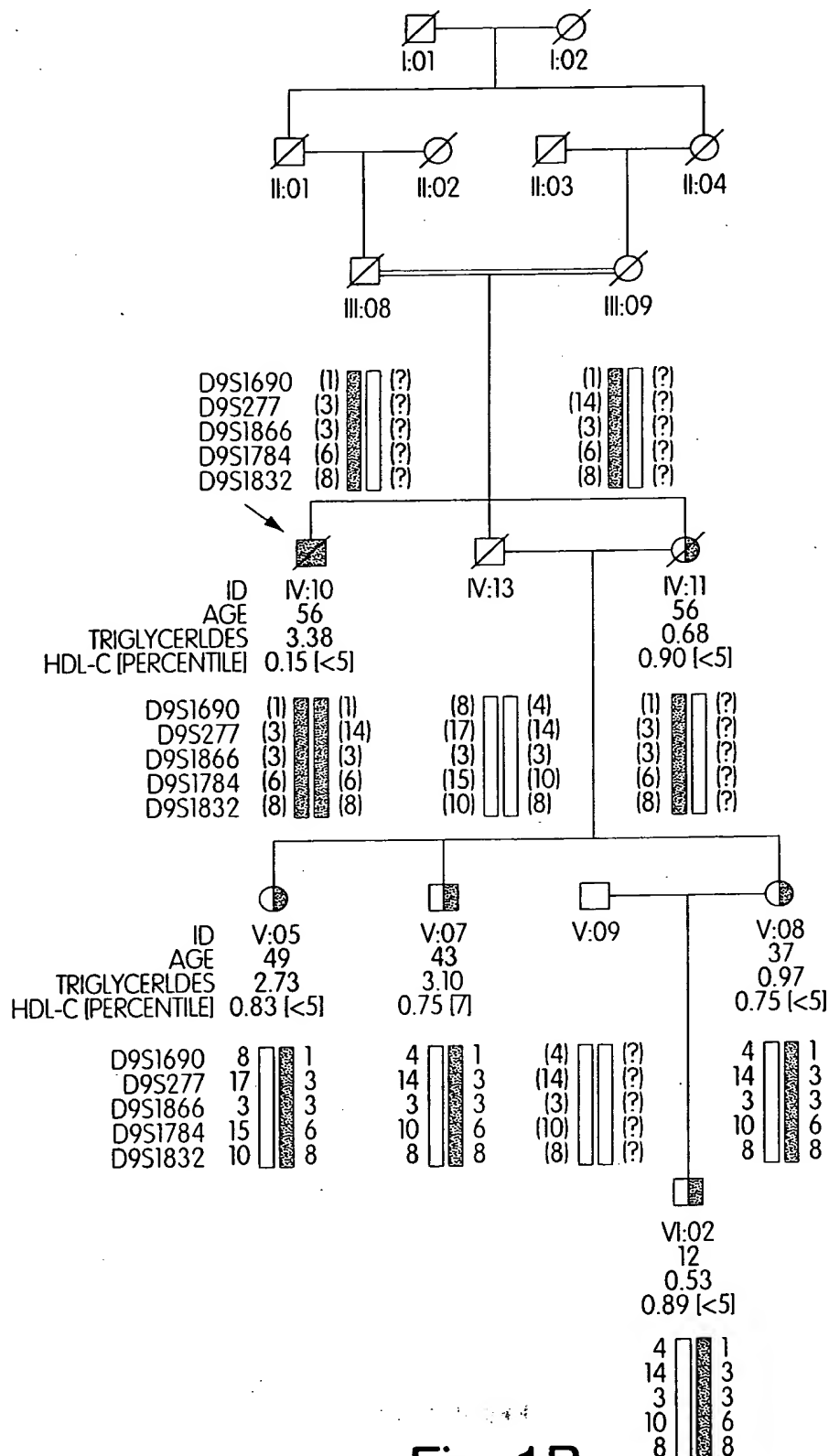


Fig. 1B

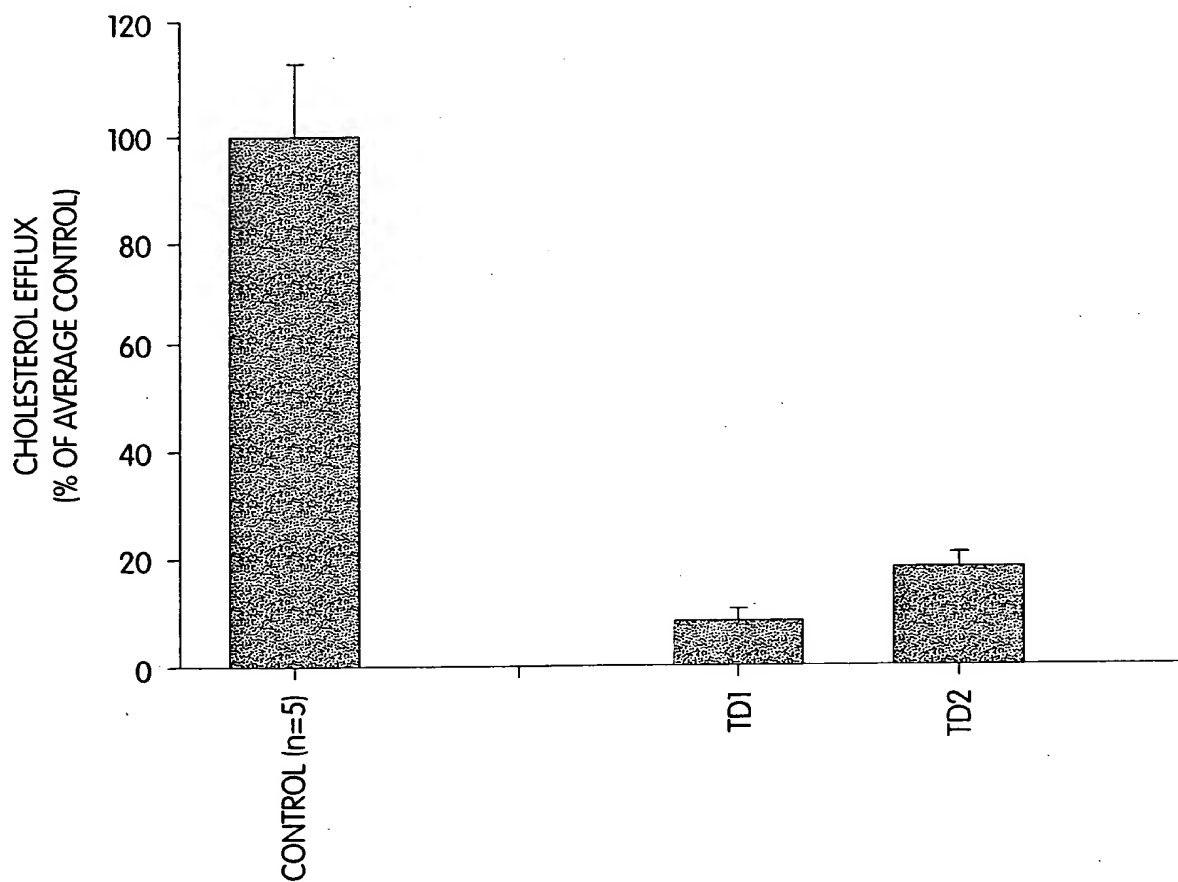


Fig. 1C



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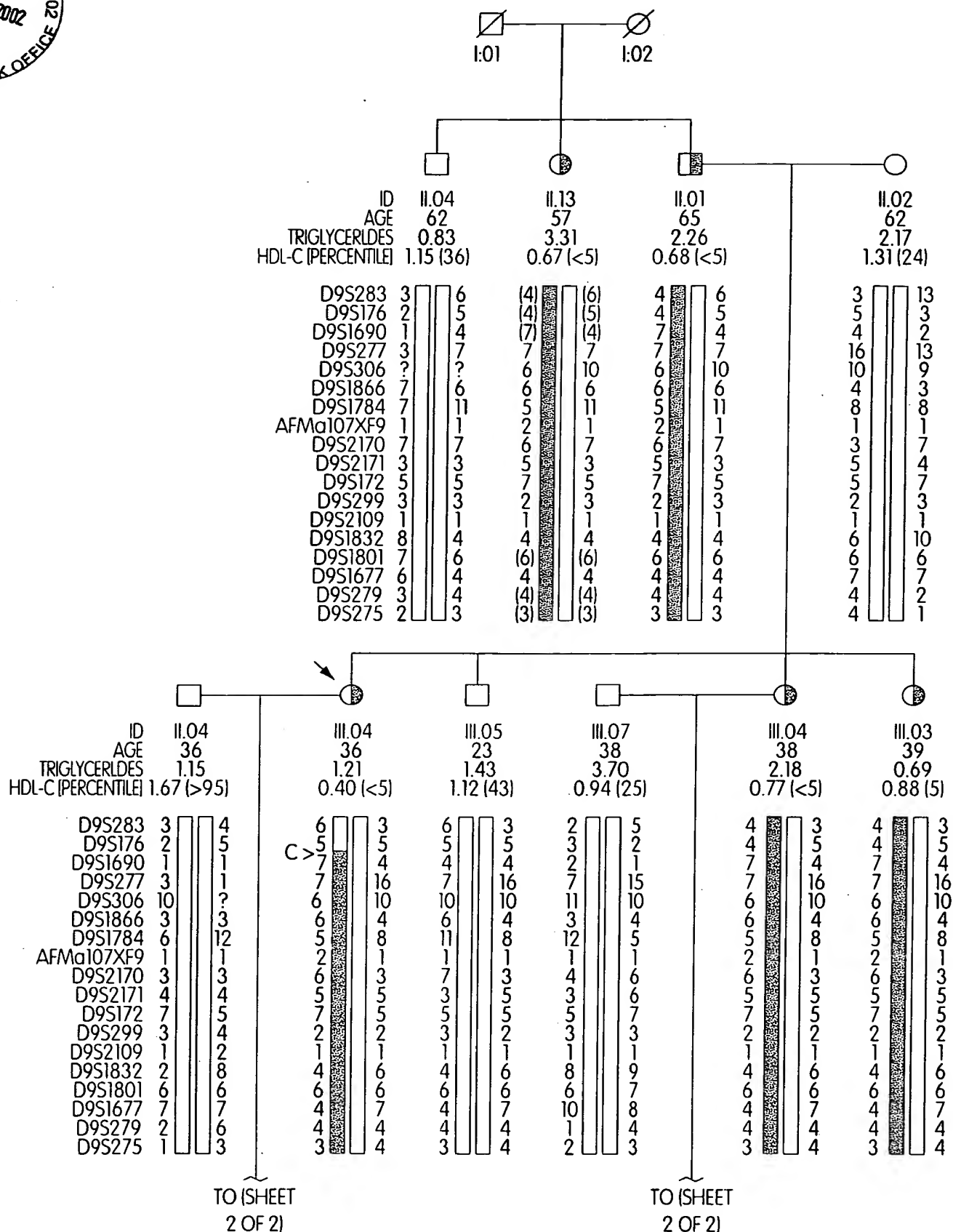


Fig. 2A (SHEET 1 OF 2)



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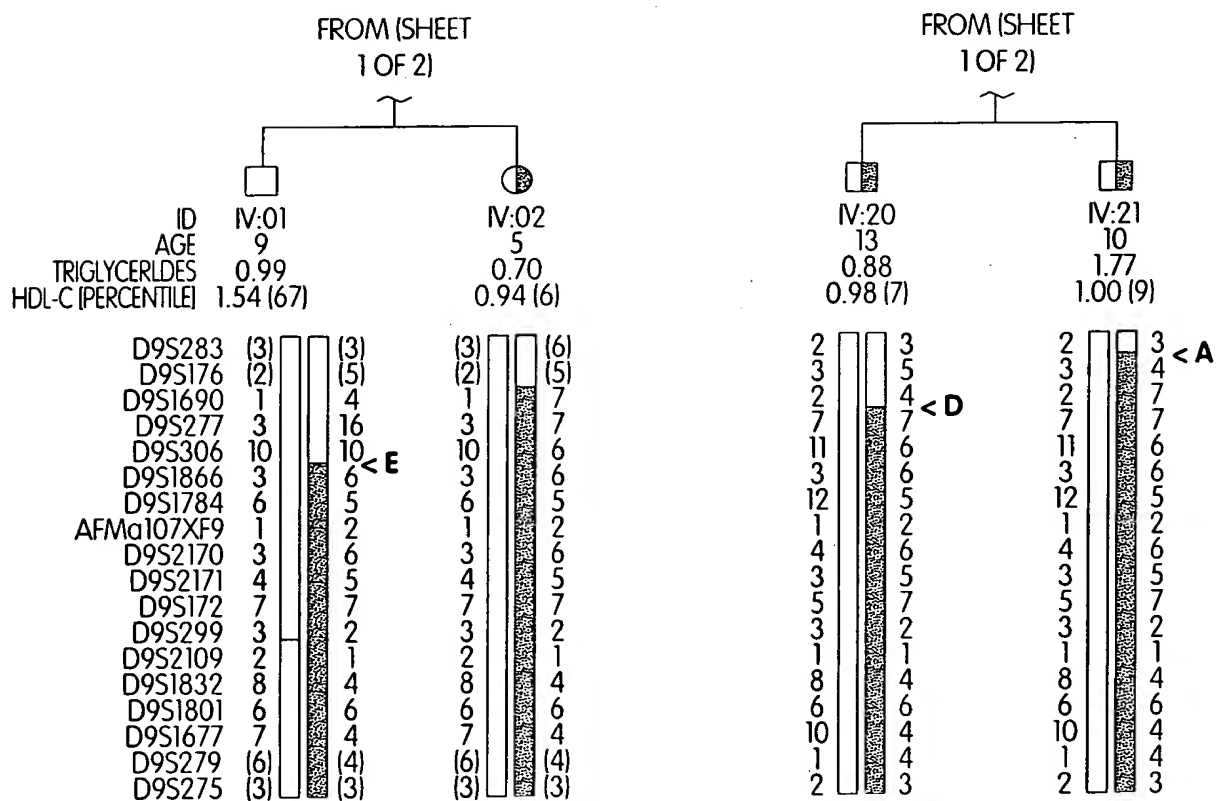
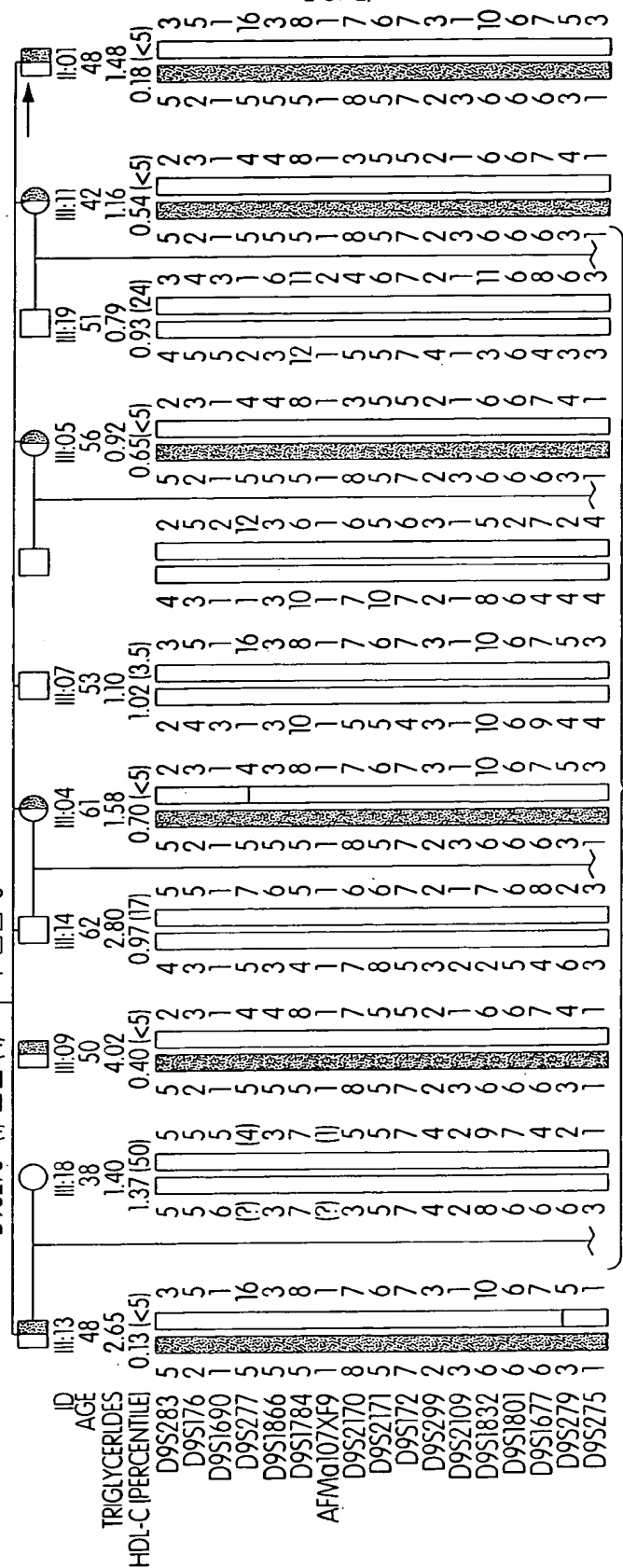
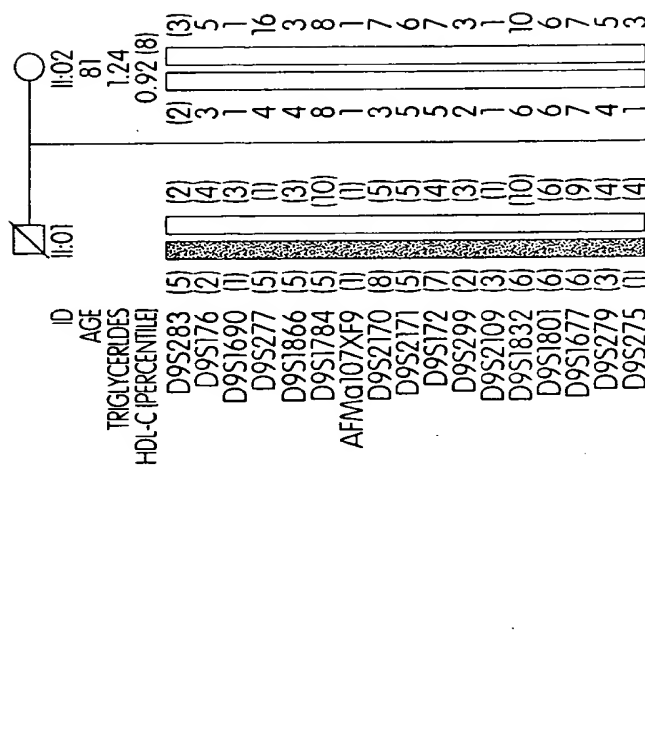


Fig. 2A (SHEET 2 OF 2)

TO (SHEET
2 OF 2)





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FROM
SHEET
1 OF 2

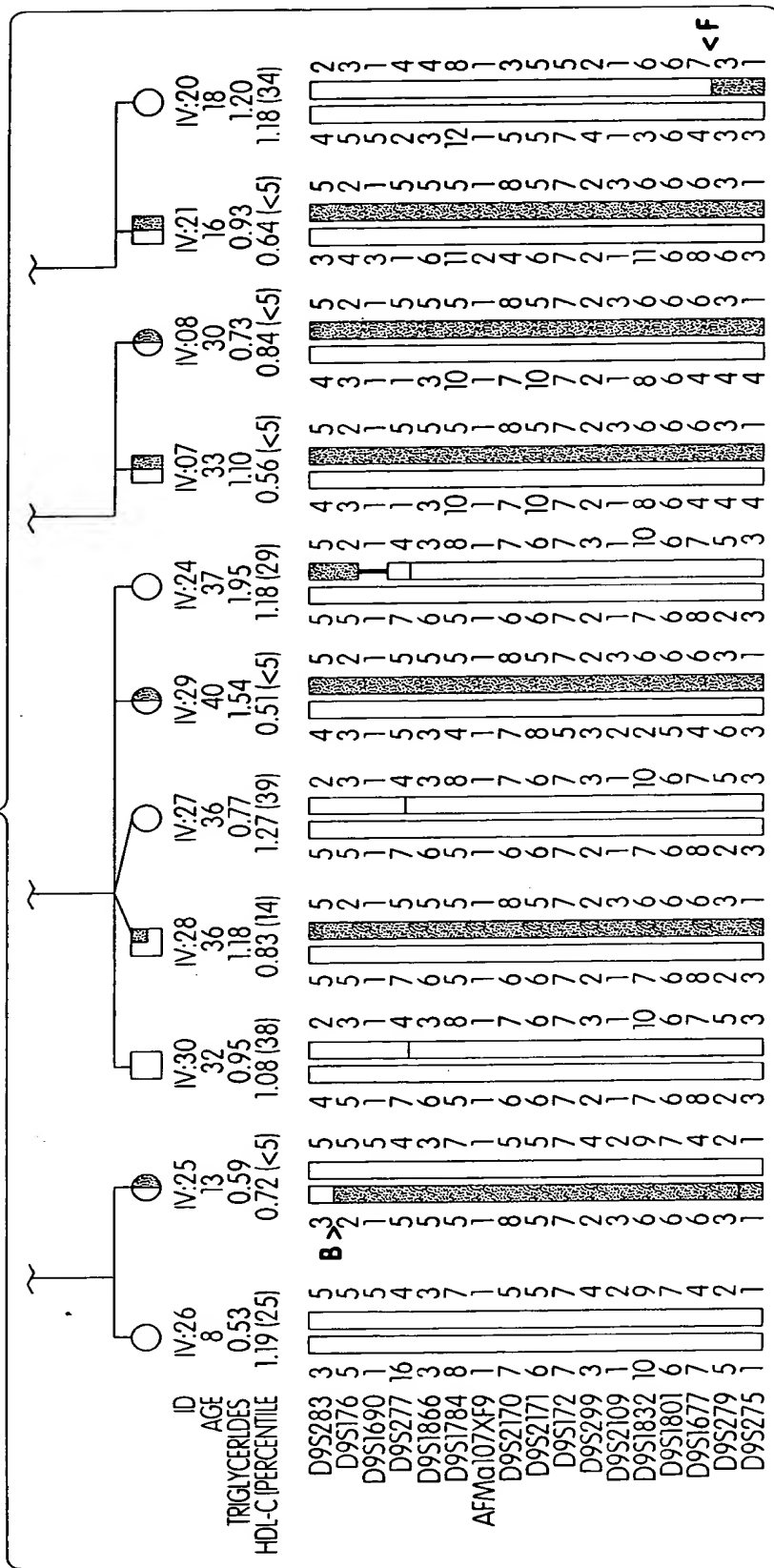


Fig. 2B (SHEET 2 OF 2)



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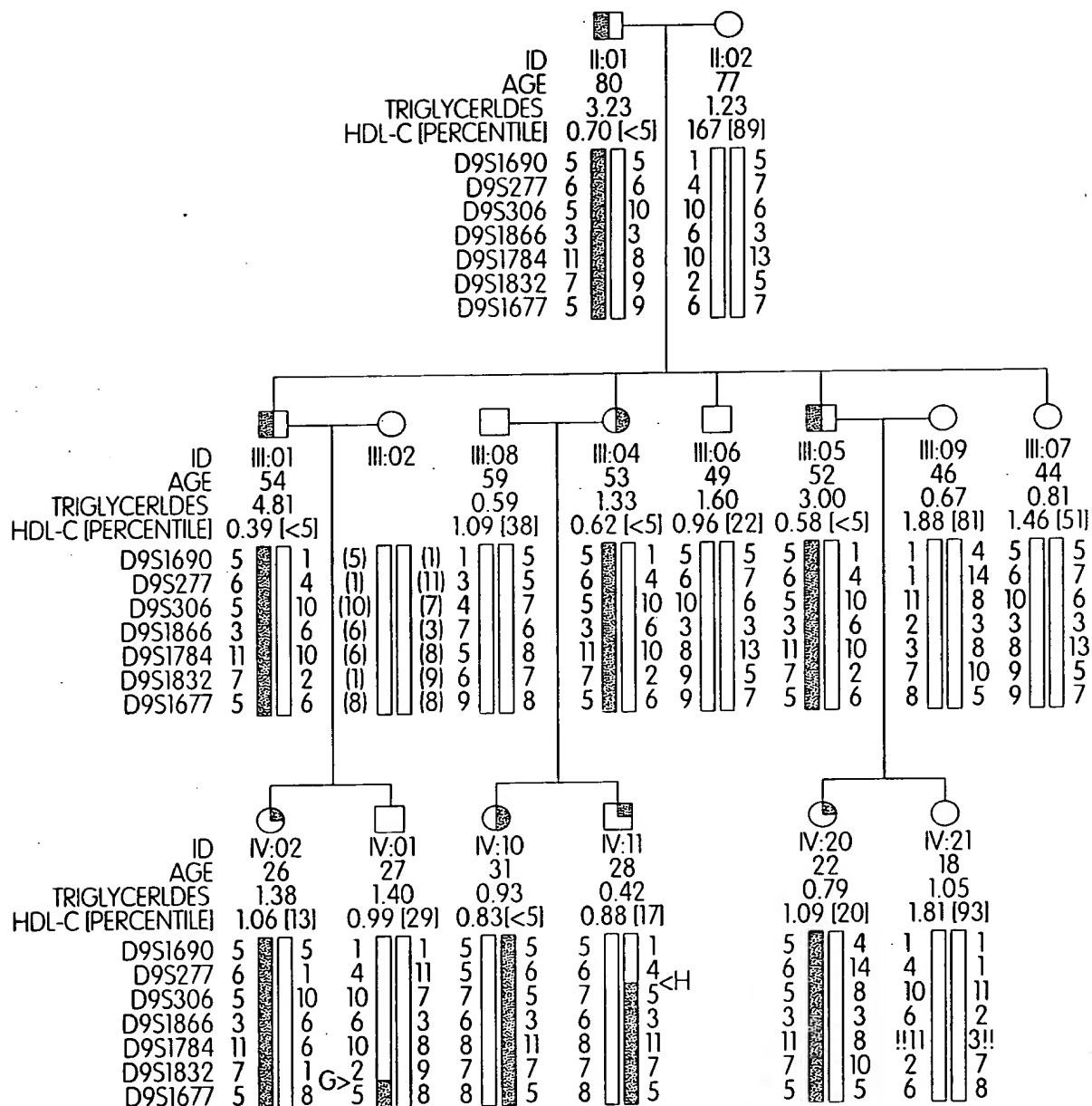


Fig. 2C

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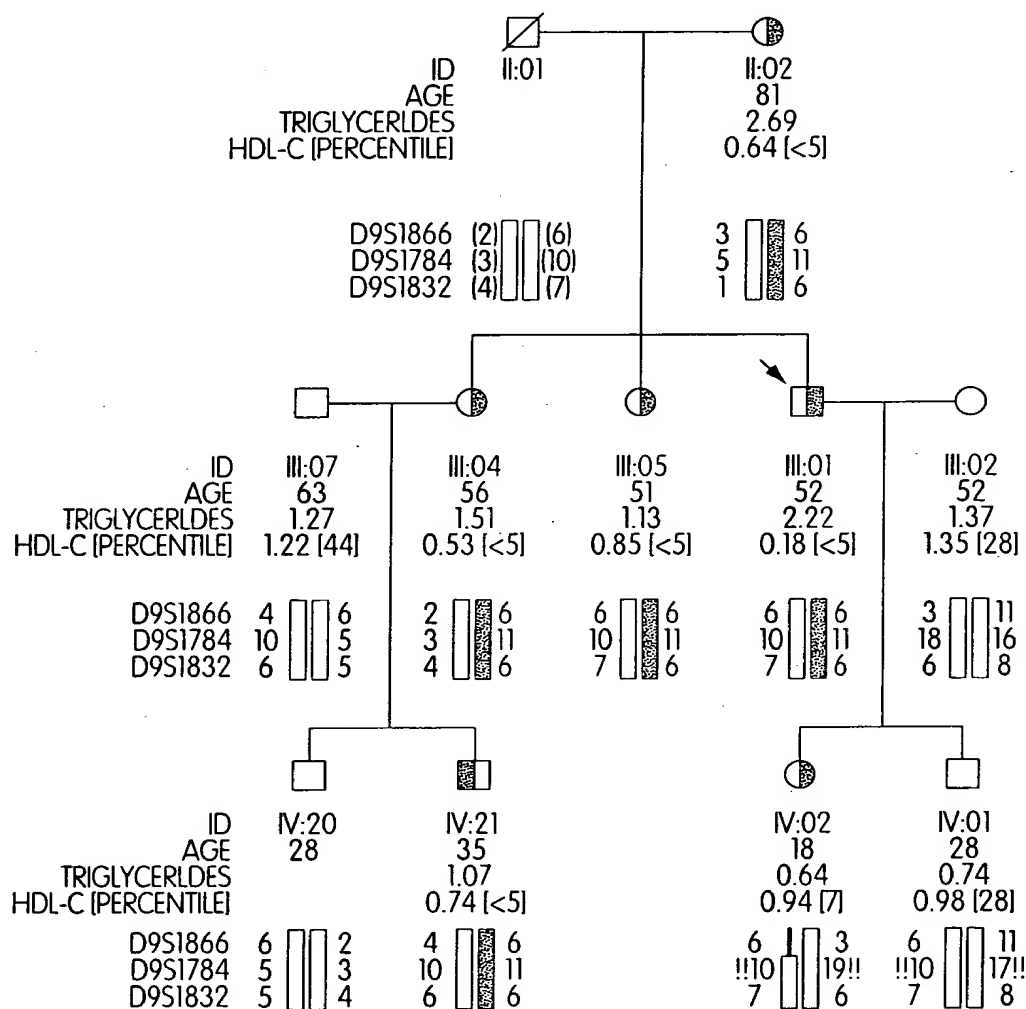


Fig. 2D



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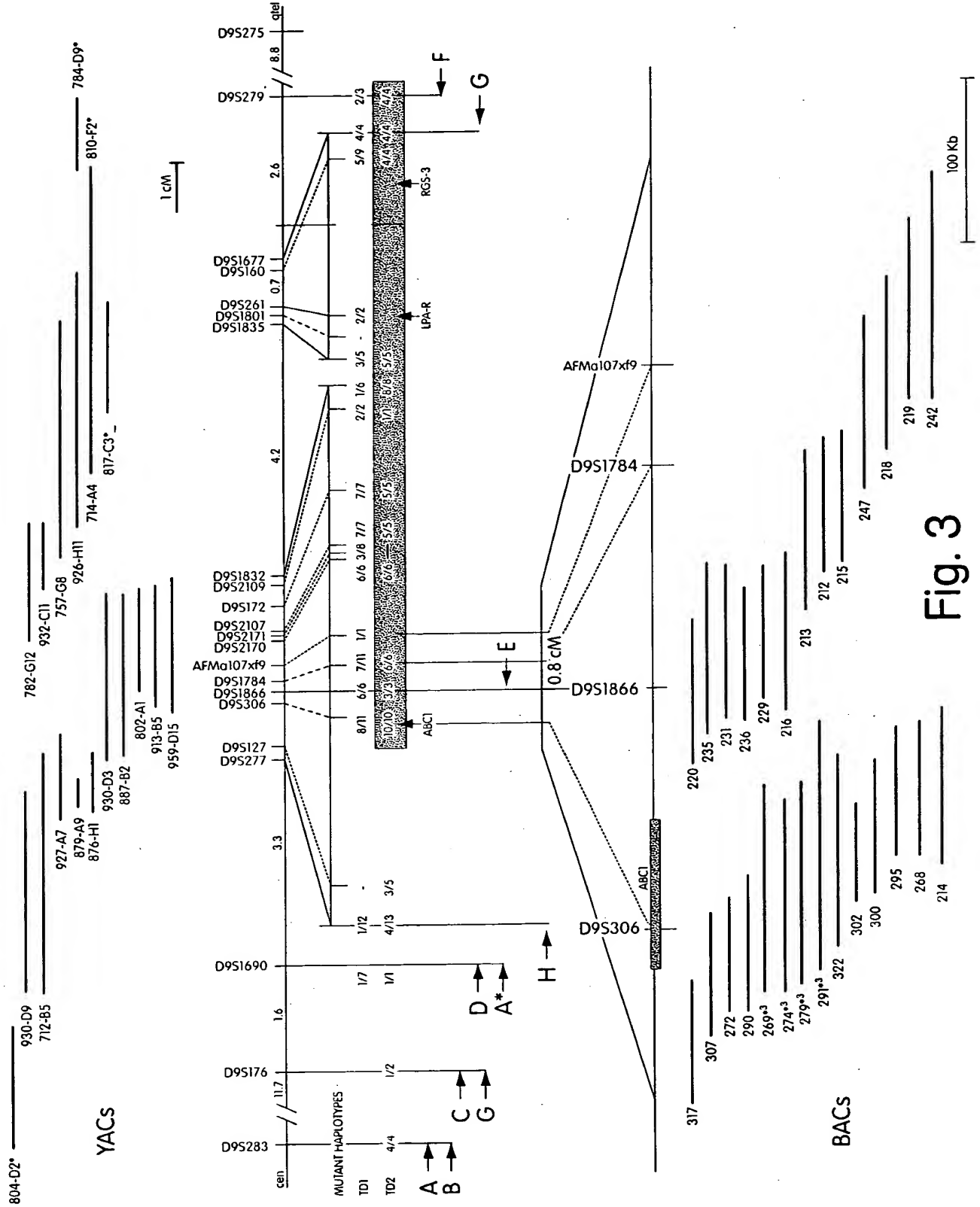


Fig. 3



Serial No.: 09/526,193
Applicant: Hayden et al
Filed: 15 March 2000
Attorney Docket: 760050-19

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EXON 20
TD-1

wt sequence
HUMAN_ABC1
MOUSE_ABC1
Patient
CAEEL_ABC
Patient

4485 4503 4529

aagaagatgctgcctgtgTgtccccccaggggacaggggggctgcct

K	K	M	L	P	V	C	P	P	G	A	G	G	L	P
K	K	M	L	P	V	C	P	P	G	A	G	G	L	P
K	K	M	L	P	V	R	P	P	G	A	G	G	L	P
-	-	L	L	-	-	-	-	-	-	-	G	G	S	-

aagaagatgctgcctgtgCgtccccccaggggacaggggggctgcct

Fig. 4B



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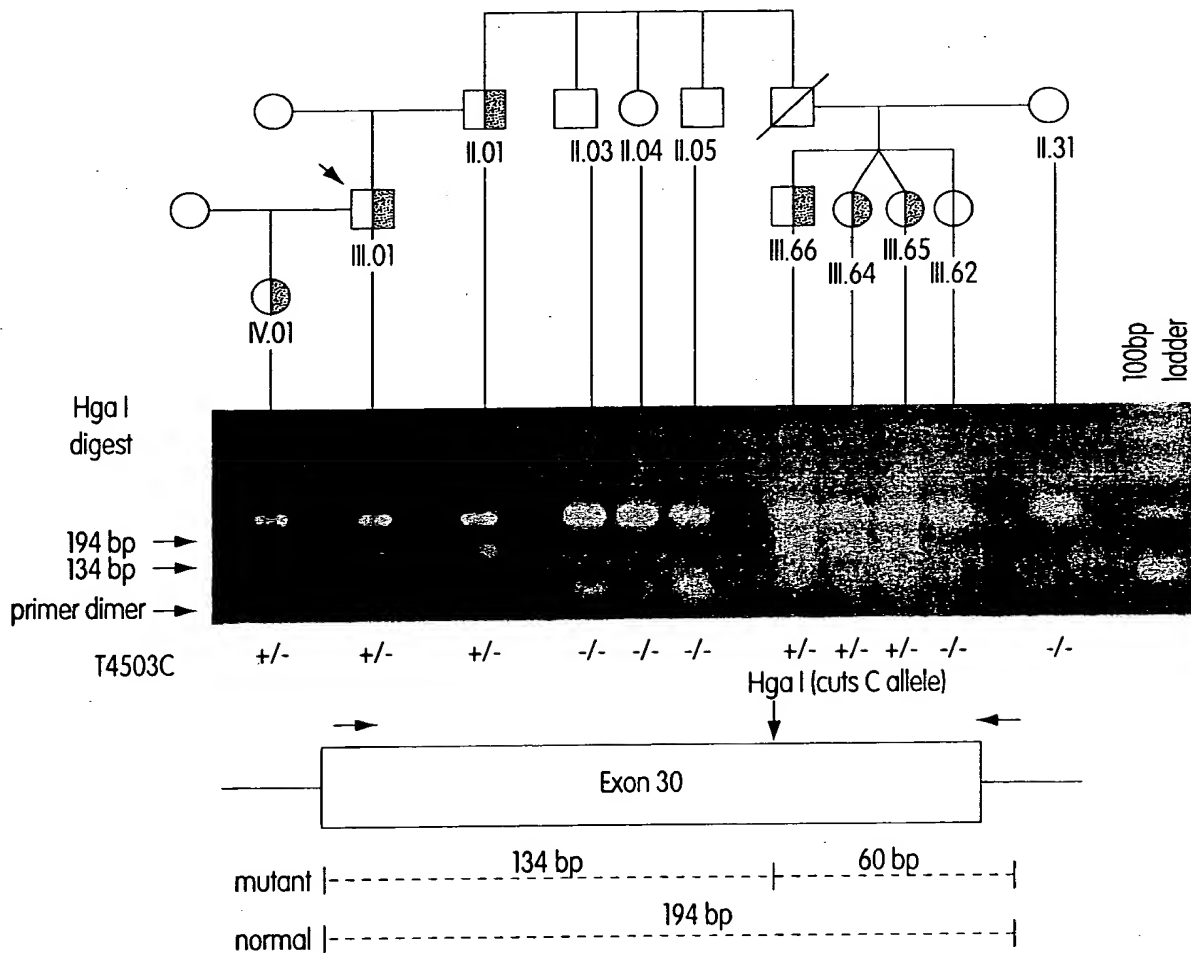


Fig. 4C



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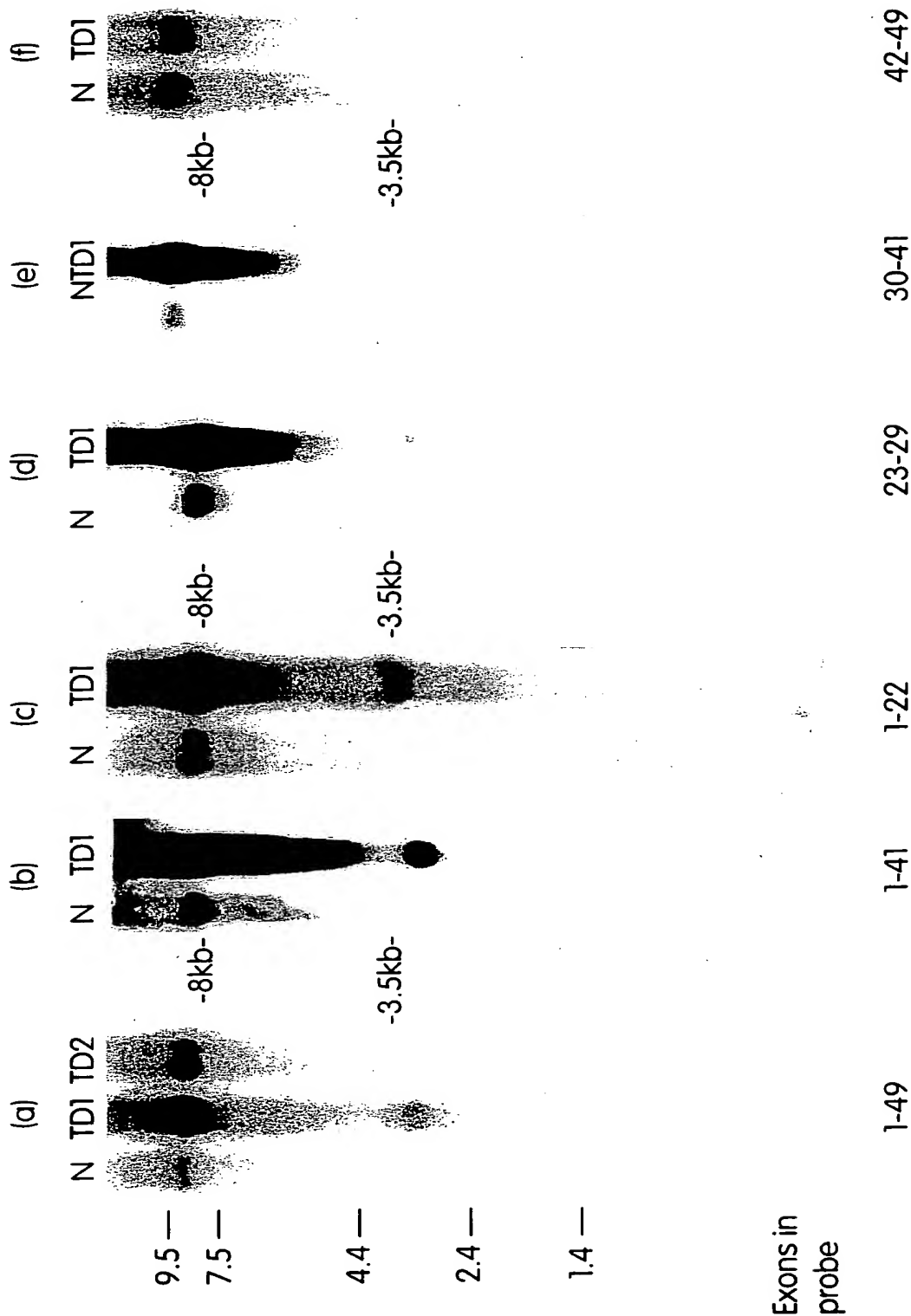


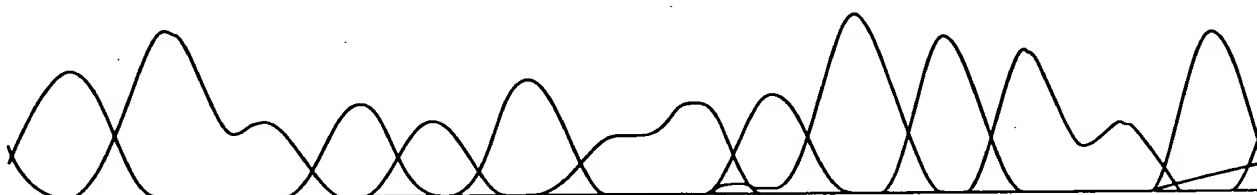
Fig. 4D



EXON 13 MUTATION:

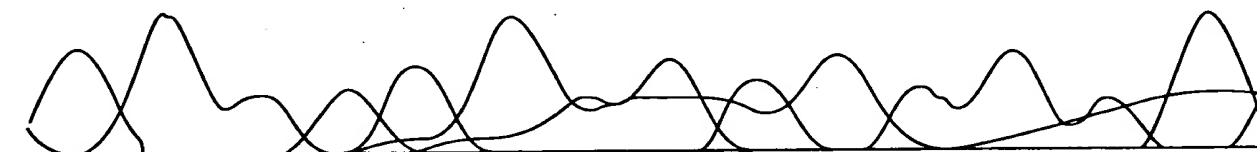
CONTROL

G C C T A C T T G C A G G A



FAMILY TD - 2, patient IV:10

G C C T A C T T G C G G G A



1854

A1864G (Q597R)

1876

Fig. 5A



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EXON 13
TD-2

wt sequence
HUMAN_ABC1
MOUSE_ABC1
Patient
CAEEL_ABC
Patient

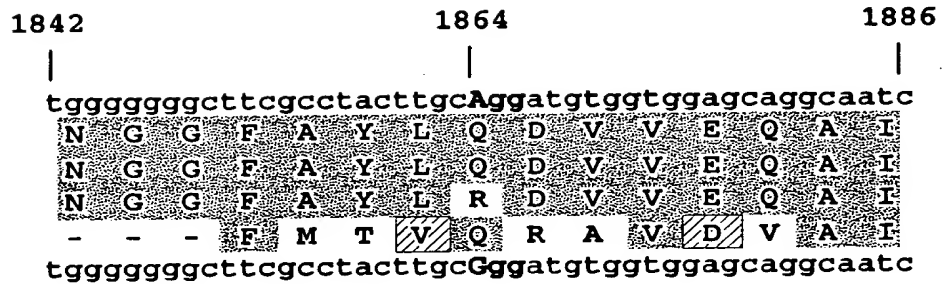
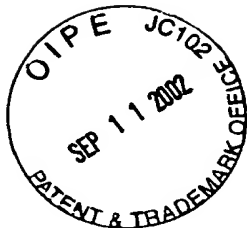


Fig. 5B



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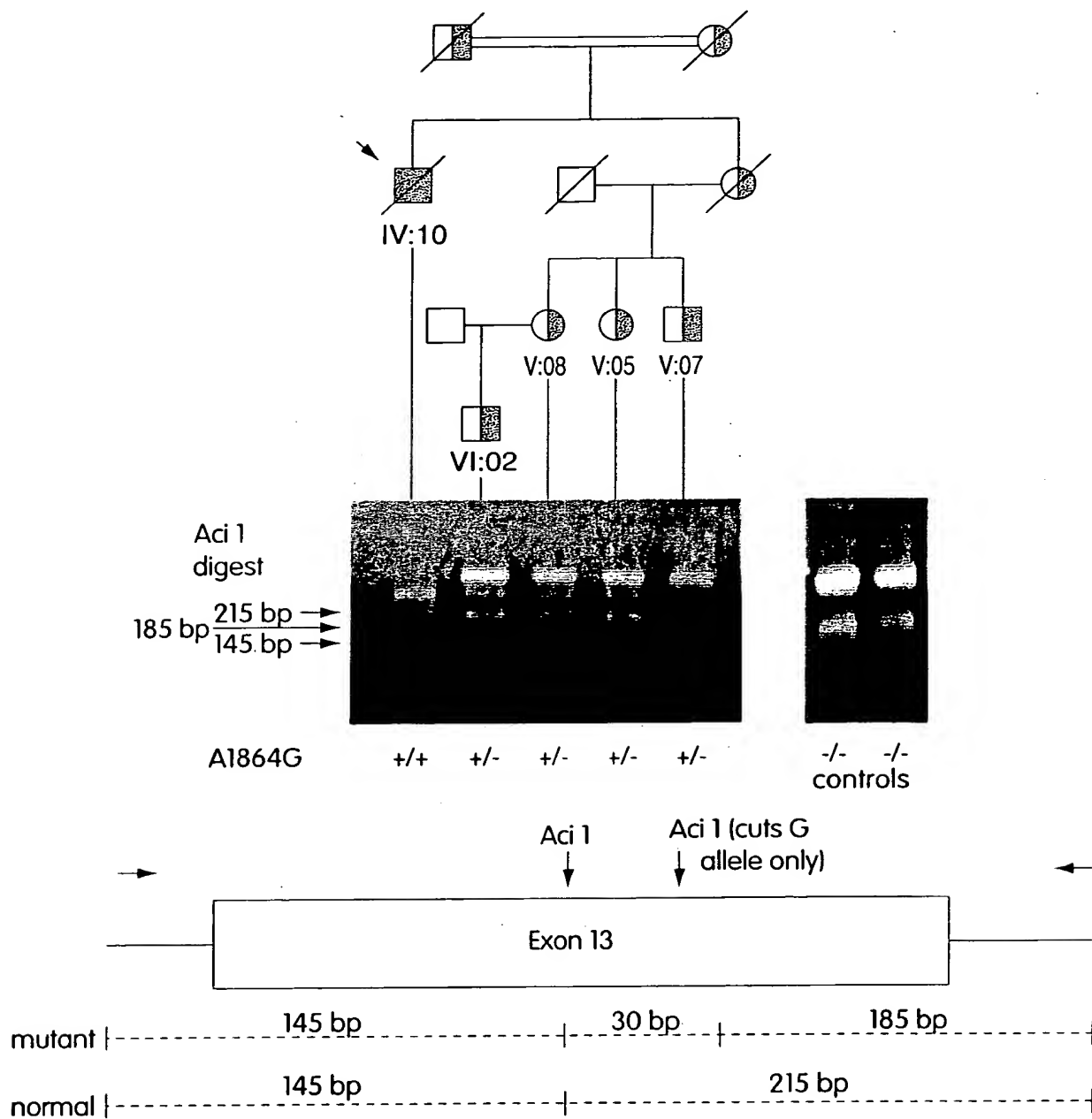


Fig. 5C



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Exon 14: FHA - 1, patient III:01

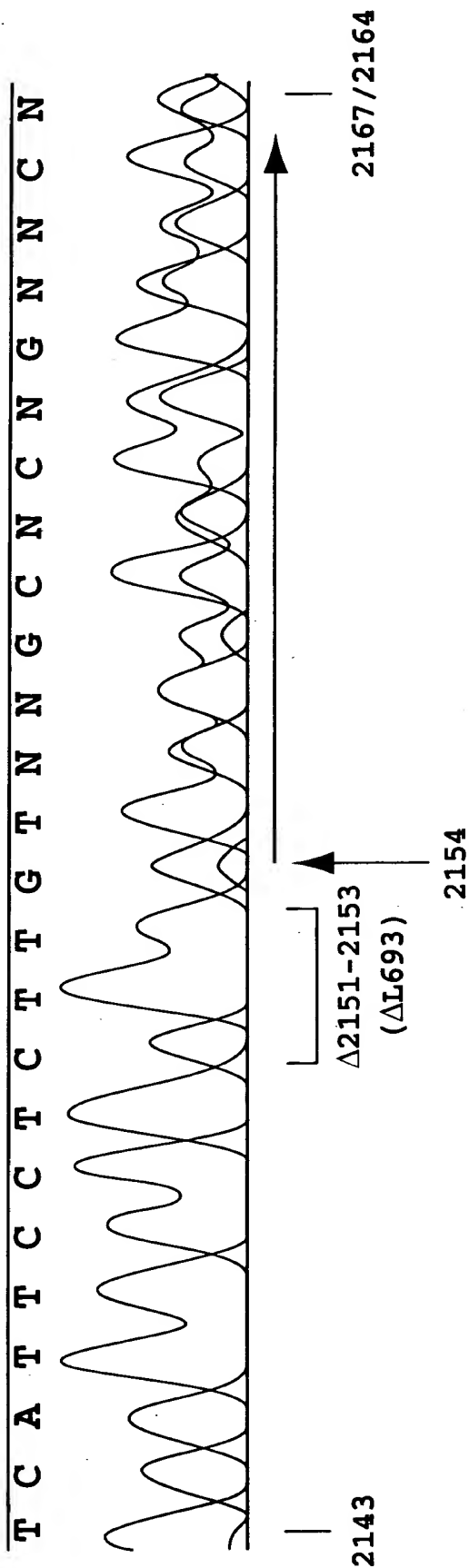


Fig. 6A



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EXON 14
FHA-1

wt sequence
HUMAN_ABC1
MOUSE_ABC1
Patient
CAEEL_ABC
Patient

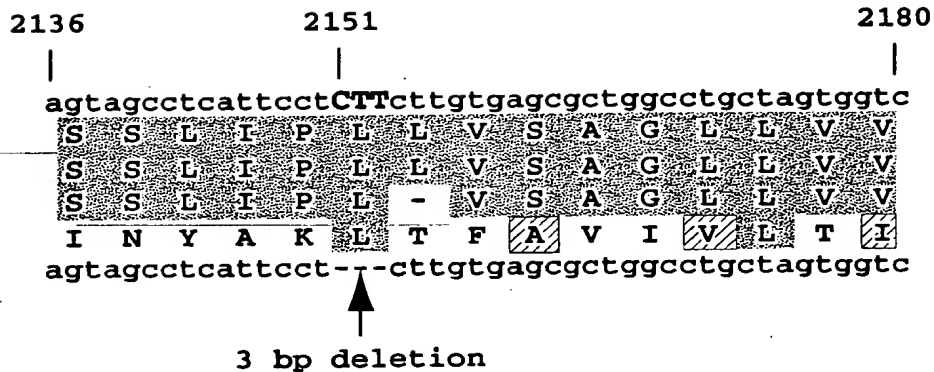


Fig. 6B

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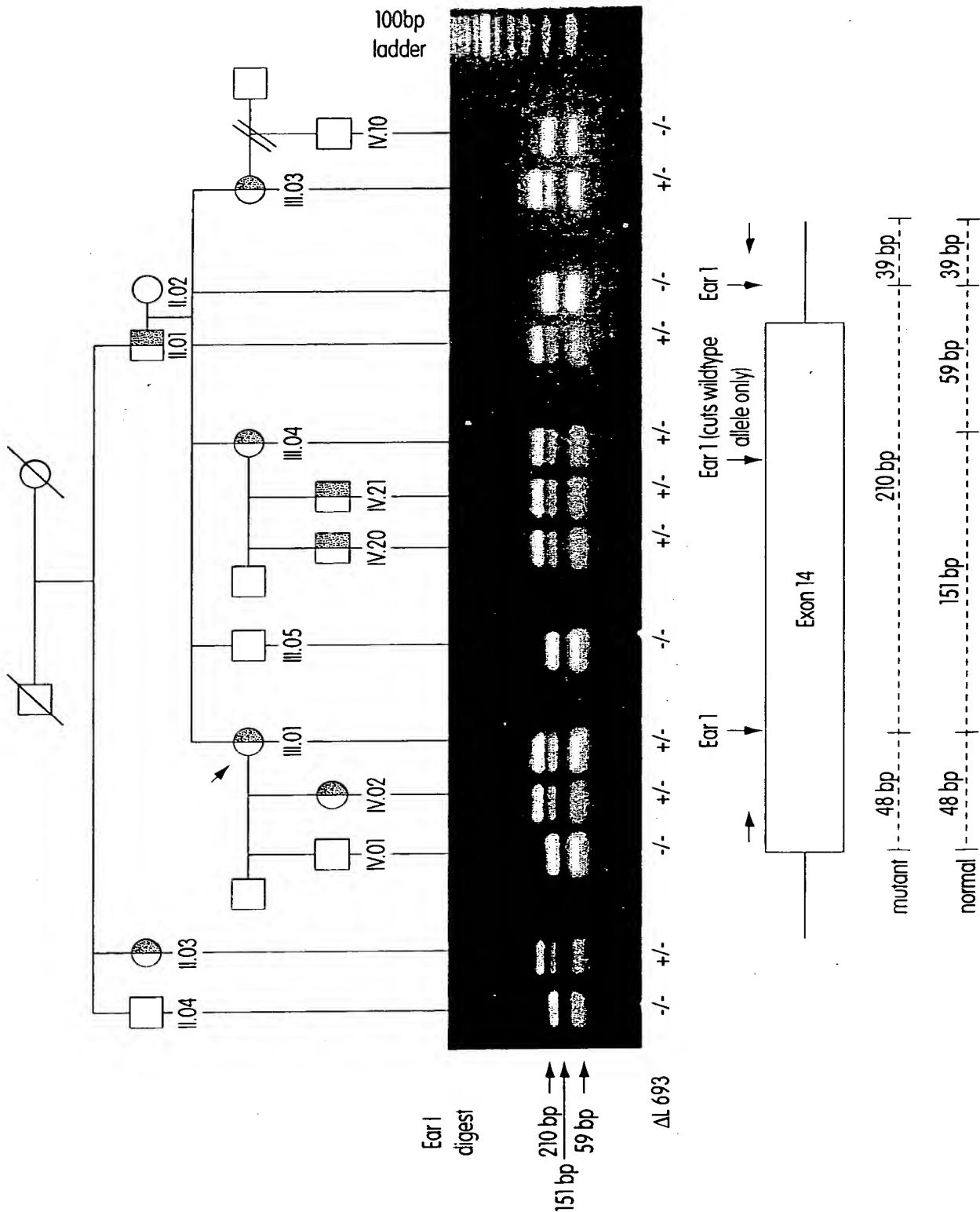


Fig. 6C



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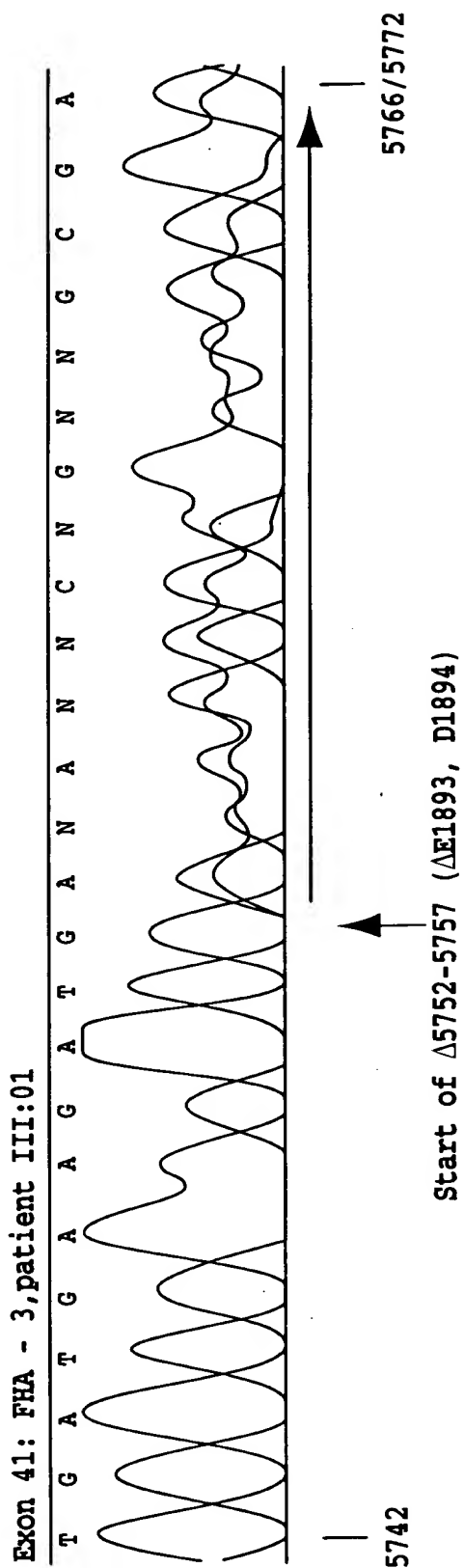


Fig. 6D



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EXON 41
FHA-3

wt sequence
HUMAN_ABC1
MOUSE_ABC1
Patient (Δ E1893, D1894)
CAEEL_ABC

Δ 5752-5757

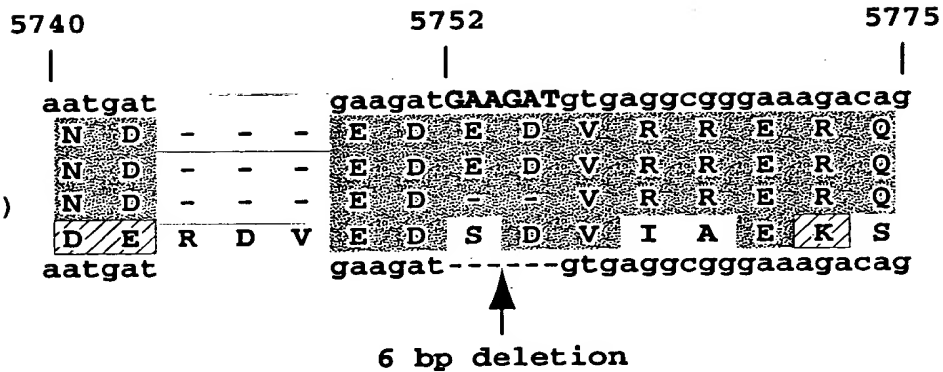


Fig. 6E



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Exon 48 mutation:

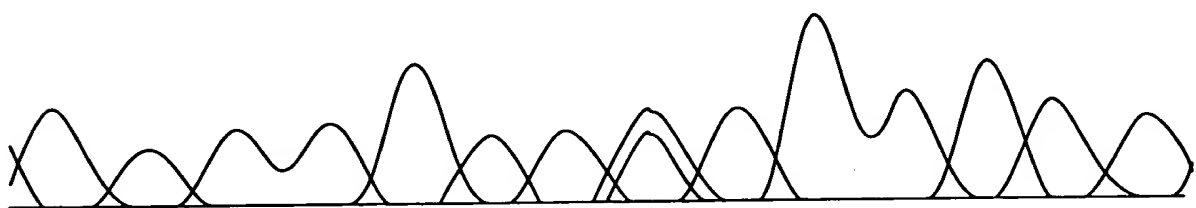
Control

A G T T G T A C G A A T A G



Family FHA - 2, patient III:01

A G T T G T A N G A A T A G



6497

C6504T (Arg2144STOP)

6510

Fig. 6F

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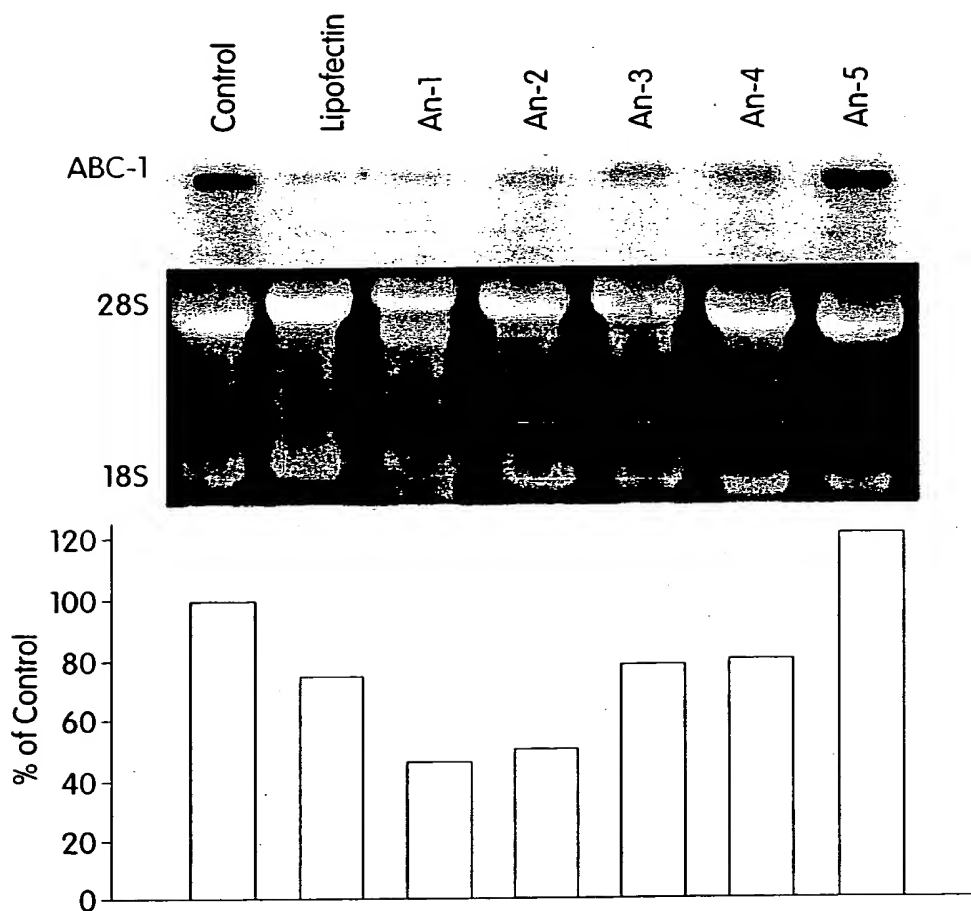


Fig. 7A

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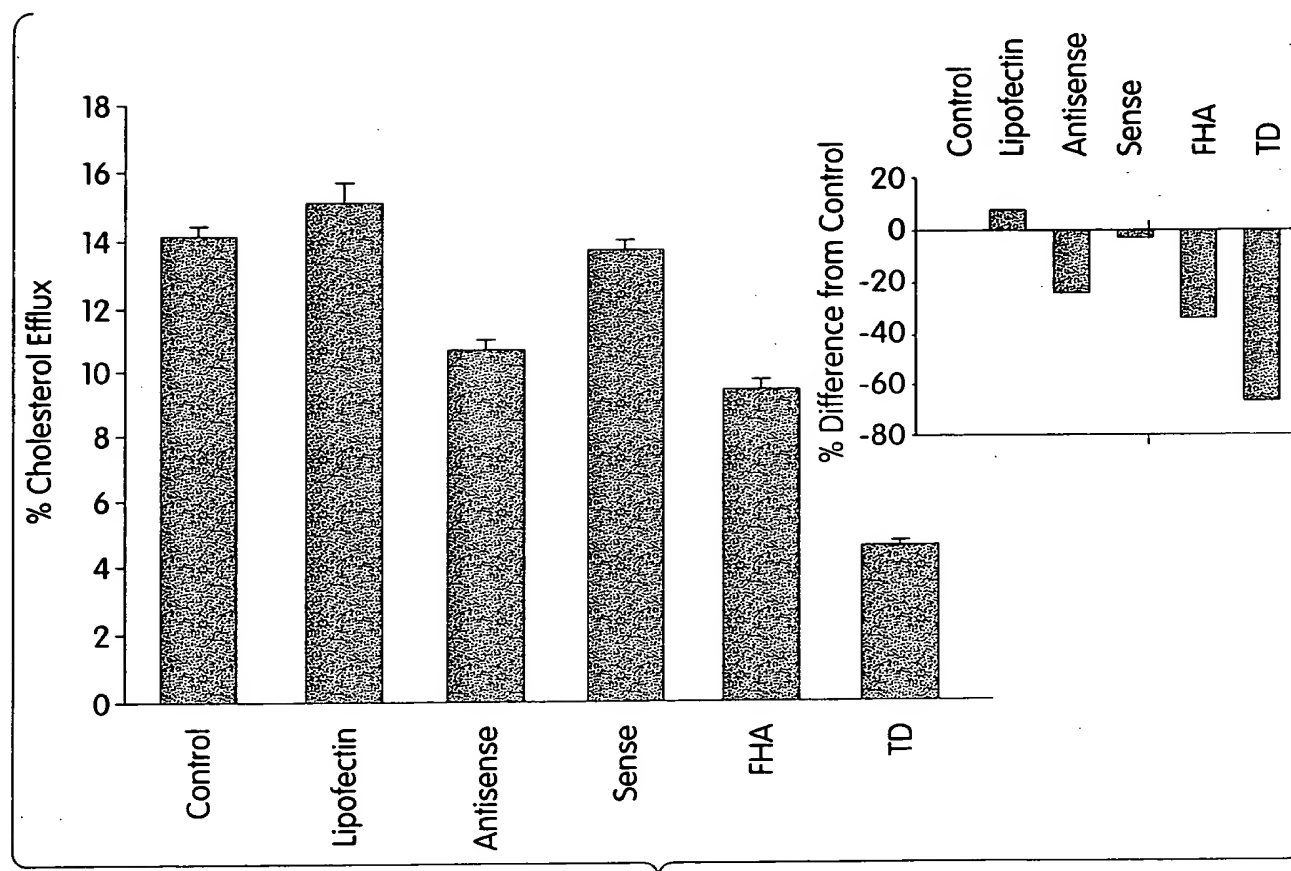


Fig. 7B



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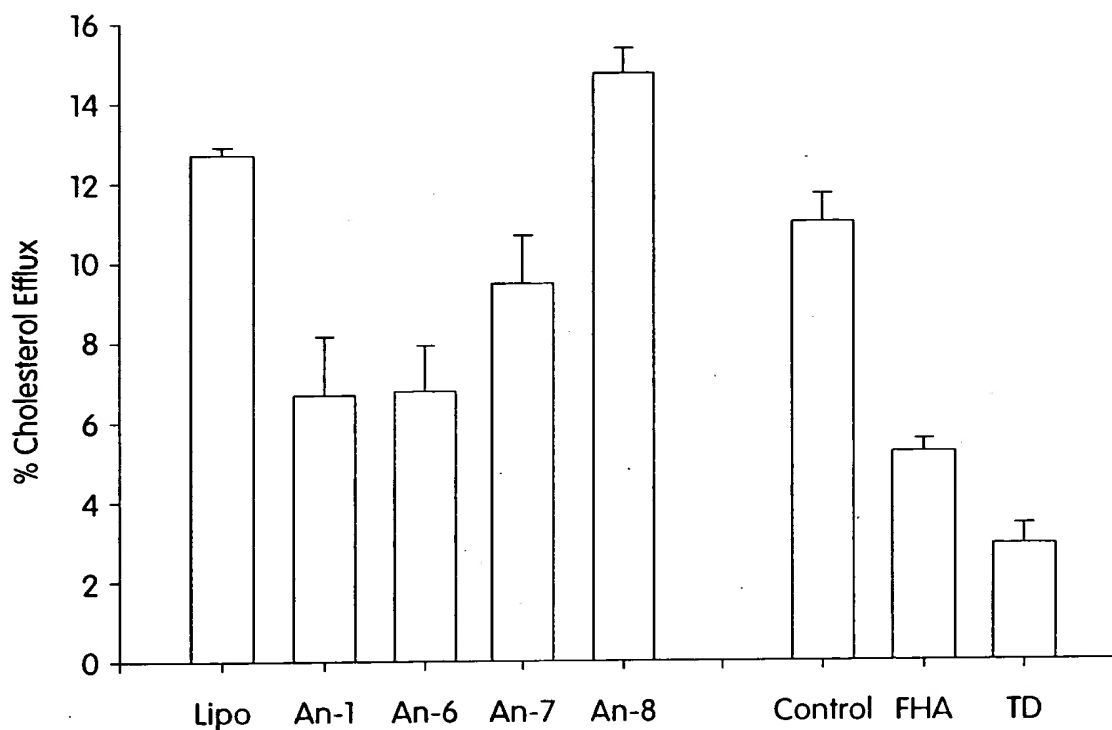
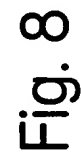


Fig. 7C



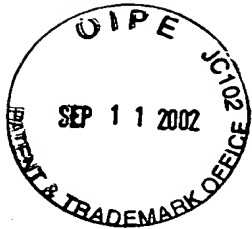


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LCGLPREKLAAAERVLRSNMDILKPIRLTLNSTSPFPSKELAEATKLLHSLGTLAQELFSMRSWSDMRQE
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NDLMKNLESSPLSRIIWKALKPLLVGKILYTPDTPATRQVMAEVNKTQELAVFHDLEGMWHEELSPKIWTF
MENSQEMDLVRMLLDSRDNDHFWEQQLDGLDWTAAQDIVAFLAKHPEDVQSSNGSVYTWREAFNETNQAIRT
ISRFMECVNLNLEPIATEVWLINKSMELLDERKFWAGIVFTGITPGSIELPHHVYKIRMDIDNVERTNK
IKDGYWDPGPRADPFEDMRYVWGGFAYLQDVVEQAIIRVLTGTEKKTGVYMQMPYPCYVDDIFLRVMSRS
MPLFMTLAWIYSVAVIIKGIYVEKEARLKETMRIMGLDNSILWFSWFISSLIPLLVSAGLLVVILKLGNNL
PYS DPSVVFVFLSVFAVVTILQCFLISTLFSRANLAAACGGIIYFTLYLPYVLCVAWQDYVGFTLKI FASL
LSPVAFGFGCEYFALFEEQGIGVQWDNL FESPVEEDGFNLTTSVSMMLFDTFLYGVMTWYIEAVFPQYGI
PRPWYFPCTKSYWFGEESDEKSHPGSNQKRRISEICMEEPTHKLGVSIQNLVKVYRDGMKVAVDGLALNF
YEQITSFLGHNGAGKTTTMSILTGLFPPTSGTAYILGKDIRSEMSTIRQNLGVCPOHNVLFDMLTVEEHI
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YSRRGIWELLKYRQGRTIILSTHMDVGLDRIAIISHGKLCVGSLLFLKNQLGTGYLTLVKKDVE
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QSCLRPFTEDDAADPNDSIDIPESRETDLISGMDGKGSYQVKGWKL TQQQFVALLWKRLLIARRSRKGFFA
QIVLPAVFVCIALVFS LIVPPFGKYPSLELQPMWYNEQYTFVSNDAPEDTGTLELLNALTKDPGFGTRCME
GNPIPDTPCQAGEEEWTTAPVPQTIMDLFQNGNWTM QNPS PACQCSSDKIKKMLPVCPPGAGGLPPPQRKQ
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GYCPQFDAITELLTGREHVEFFALLRGVPEKEVGKVGWEAIRKLGVLKYGEKYAGNYS GGNKRKLSTAMAL
IGGPPVVFLDEPTTGMDPKARRFLWNCALS VVKEGRSVVLTSHSMEECEALCTMAIMVNGRFRCLGSVQH
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Fig. 9A



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SEQ ID NO: 2

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CTGGCTGAGGGAACATGGCTTGTGGCCCTCAGCTGAGGTTGCTGCTGTGGAAGAACCCTCA
CTTTCAGAAGAAGACAAACATGTCAGCTGTTACTGGAAGTGGCCTGGCCTCTATTTATCT
TCCTGATCCTGATCTCTGTTCCGGCTGAGCTACCCACCCCTATGAACAACATGAATGCCATT
TTCCAAATAAAGCCATGCCCTCTGCAGGAACACTTCCTTGGGTTTCAGGGGATTATCTGTA
ATGCCAACAACCCCTGTTTCCGTTACCCGACTCCTGGGGAGGCTCCCGGAGTTGTTGGAA
ACTTTAACAATCCATTGTGGCTCGCCTGTTCTCAGATGCTCGGAGGCTTCTTTTATACA
GCCAGAAAGACACCAGCATGAAGGACATGCGCAAAGTTCTGAGAACATTACAGCAGATCA
AGAAATCCAGCTCAAACCTGAAGCTTCAAGATTTCCTGGTGGACAATGAAACCTTCTCTG
GGTTCCTGTATCACAACCTCTCTCTCCCAAAGTCTACTGTGGACAAGATGCTGAGGGCTG
ATGTCATTCTCCACAAGGTATTTTTCGAAGGCTACCAGTTACATTTGACAAGTCTGTGCA
ATGGATCAAAATCAGAAGAGATGATTCAACTTGGTGACCAAGAAGTTCTGAGCTTTGTG
GCCTACCAAGGGAGAACTGGCTGCAGCAGAGCGAGTACTTCGTTCCAACATGGACATCC
TGAAGCCAATCCTGAGAACATAAACTCTACATCTCCCTTCCCGAGCAAGGAGCTGGCTG
AAGCCACAAAAACATTGCTGCATAGTCTTGGGACTCTGGCCCAGGAGCTGTTTCAGCATGA
GAAGCTGGAGTGACATGCGACAGGAGGTGATGTTTCTGACCAATGTGAACAGCTCCAGCT
CCTCCACCCAAATCTACCAGGCTGTGTCTCGTATTGTCTGCGGGCATCCCGAGGGAGGGG
GGCTGAAGATCAAGTCTCTCAACTGGTATGAGGACAACAACATACAAAGCCCTCTTTGGAG
GCAATGGCACTGAGGAAGATGCTGAAACCTTCTATGACAACCTCTACAACCTCTTACTGCA
ATGATTTGATGAAGAATTTGGAGTCTAGTCTCTTTTCCCGCATTATCTGGAAGCTCTGA
AGCCGCTGCTCGTTGGGAAGATCCTGTATACACCTGACACTCCAGCCACAAGGCAGGTCA
TGGCTGAGGTGAACAAGACCTTCCAGGAAGTGGCTGTGTTCCATGATCTGGAAGGCATGT
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TCCGGATGCTGTTGGACAGCAGGGACAATGACCACTTTTGGGAACAGCAGTTGGATGGCT
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CCAGTAATGGTTCTGTGTACACCTGGAGAGAAGCTTTCAACGAGACTAACCCAGGCAATCC
GGACCATACTCGCTTCATGGAGTGTGTCAACCTGAACAAGCTAGAACCCATAGCAACAG
AAGTCTGGCTCATCAACAAGTCCATGGAGCTGCTGGATGAGAGGAAGTTCTGGGCTGGTA
TTGTGTTCACTGGAATTACTCCAGGCAGCATTGAGCTGCCCCATCATGTCAAGTACAAGA
TCCGAATGGACATTGACAATGTGGAGAGGACAAATAAAATCAAGGATGGGTACTGGGACC
CTGGTCTCGAGCTGACCCCTTTGAGGACATGCGGTACGTCTGGGGGGGCTTCGCCTACT
TGCAGGATGTGGTGGAGCAGGCAATCATCAGGGTGTGACGGGCACCGAGAAGAAAACCTG

Fig. 9B



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GTGTCATATATGCAACAGATGCCCTATCCCTGTTACGTTGATGACATCTTCTGCGGGTGA
TGAGCCGGTCAATGCCCTCTTTCATGACGCTGGCTGGATTTACTCAGTGGCTGTGATCA
TCAAGGGCATCGTGATGAGAAGGAGGCACGGCTGAAAGAGACCATGCGGATCATGGGCC
TGGACAACAGCATCCCTGTTTGTAGCTGGTTTATTAGTAGCCTCATTCCTCTTCTTGTGA
GCGCTGGCTGCTAGTGGTCACTCTGAAGTTAGGAAACCTGCTGCCCTACAGTGATCCCA
GCGTGGTGTGTTGCTTCCCTGTCCGTGTTTGTGTGGTGACAATCCTGCAGTGCTTCCCTGA
TTAGCACACTCTTCTCCAGAGCCAACCTGGCAGCAGCCTGTGGGGGCATCATCTACTTCA
CGCTGTACCTGCCCTACGTCCCTGTGTGTGGCATGGCAGGACTACGTGGGCTTCACACTCA
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GGGTGATGACCTGGTACATTGAGGCTGTCTTTCCAGGCCAGTACGGAATTTCCAGGCCCT
GGTATTTTCCTTGCACCAAGTCCCTACTGGTTTGGCGAGGAAAGTGATGAGAAGAGCCACC
CTGGTTCCAACCAGAAGAGAAATATCAGAAATCTGCATGGAGGAGGAACCCACCCACTTGA
AGCTGGGCGTGTCCATTTCAGAACCTGGTAAAGTCTACCGAGATGGGATGAAGGTGGCTG
TCGATGGCTGGCACTGAATTTTTATGAGGGCCAGATCACCTCCTTCCCTGGGCCACAATG
GAGCGGGGAAGACGACCACCATGTCAATCCTGACCGGGTTGTTCCCCCGACCTCGGGCA
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TCTATGCCCCGCTTGAAAGGGCTCTCTGAGAAGCACGTGAAGCGGAGATGGAGCAGATGG
CCCTGGATGTTGGTTTGCCATCAAGCAAGCTGAAAAGCAAAACAAGCCAGCTGTCAGGTG
GAATGCAGAGAAAGCTATCTGTGGCCTTGGCCTTTGTGCGGGGATCTAAGGTTGTCTATC
TGGATGAACCCACAGCTGGTGTGGACCTTACTCCCGCAGGGGAATATGGGAGCTGCTGC
TGAAATACCGACAAGGCCCGACCATTTCTCTCTACACACCACATGGATGAAGCGGACG
TCCTGGGGGACAGGATTGCCATCATCTCCCATGGGAAGCTGTGCTGTGTGGGCTCCTCCC
TGTTTCTGAAGAACCAGCTGGGAACAGGCTACTACCTGACCTTGGTCAAGAAAGATGTGG
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TGACCATCGATGTCTCTGCTATCTCCAACCTCATCAGGAAGCATGTGTCTGAAGCCCCGGC
TGGTGGAAGACATAGGGCATGAGCTGACCTATGTGCTGCCATATGAAGCTGCTAAGGAGG
GAGCCTTTGTGGAACCTTTTCATGAGATTGATGACCGCTCTCAGACCTGGGCATTTCTA
GTTATGGCATCTCAGAGACGACCTTGAAGAAATATTCCTCAAGGTGGCCGAAGAGAGTG
GGGTGGATGCTGAGACCTCAGATGGTACCTTGCCAGCAAGACGAAACAGGCGGGCCTTCG
GGGACAAGCAGAGCTGTCTTCGCCCGTTCACTGAAGATGATGCTGCTGATCCAAATGATT

Fig. 9C



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CTGACATAGACCCAGAATCCAGAGAGACAGACTTGCTCAGTGGGATGGATGGCAAAGGGT
CCTACCAGGTGAAAGGCTGGAACTTACACAGCAACAGTTTGTGGCCCTTTTGTGGAAGA
GACTGCTAATTGCCAGACGGAGTCGGAAGGATTTTTTGCTCAGATTGTCTTGCCAGCTG
TGTTTGTCTGCATTGCCCTTGTGTTACAGCTGATCGTGCCACCCTTTGGCAAGTACCCCA
GCCTGGAACCTCAGCCCTGGATGTACAACGAACAGTACACATTTGTCAGCAATGATGCTC
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TGCAGAACCCTTCACCTGCATGCCAGTGTAGCAGCGACAAAATCAAGAAGATGCTGCCTG
TGTGTCCCCCAGGGGCAGGGGGCTGCCTCCTCCACAAAGAAAACAAAACACTGCAGATA
TCCTTCAGGACCTGACAGGAAGAAACATTTCCGATTATCTGGTGAAGACGTATGTGCAGA
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GCTTGGGAAGATTTATGACAGGACTGGACACCAGAAATAATGTCAAGGTGTGGTTCAATA
ACAAGGGCTGGCATGCAATCAGCTCTTTCCTGAATGTCATCAACAATGCCATTCTCCGGG
CCAACCTGCAAAAGGGAGAGAACCCTAGCCATTATGGAATTACTGCTTTCAATCATCCCC
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TGATCCAGGAGCGGGTCAGCAAAGCAAAACACCTGCAGTTCATCAGTGGAGTGAAGCCTG
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GGGAGAATCGCTTTGTGTCACCATTATCTTGGGACTTGGTGGGACGAAACCTCTTCGCCA
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TTCTCCTGGTGAGTGCTTTGGGCTCCTGGGAGTTAATGGGGCTGGAAATCATCAACTT
TCAAGATGTTAACAGGAGATACCACTGTTACCAGAGGAGATGCTTTCCTTAACAAAAATA

Fig. 9D

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GTATCTTATCAAAACATCCATGAAGTACATCAGAACATGGGCTACTGCCCTCAGTTTGATG
CCATCACAGAGCTGTTGACTGGGAGAGAACACGTGGAGTTCTTTGCCCTTTTGAGAGGAG
TCCAGAGAAAAGATTGGCAAGGTTGGTGAGTGGGCGATTTCGAAACTGGGCCTCGTGA
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CCATGGCTTTGATCGGCGGGCCTCCTGTGGTGTCTTGATGAACCCACCACAGGCATGG
ATCCCAAAGCCCGCGGTTCTTGTGGAATTTGTGCCCTAAGTGTGTCAAGGAGGGGAGAT
CAGTAGTGCTTACATCTCATAGTATGGAAGAATGTGAAGCTCTTTGCACTAGGATGGCAA
TCATGGTCAATGGAAGGTTCAAGTGCCCTTGGCAGTGTCCAGCATCTAAAAAATAGGTTTG
GAGATGGTTATACAATAGTTGTACGAATAGCAGGGTCCAACCCGGACCTGAAGCCTGTCC
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TATTTGTGAACTTTGCCAAGGACCAAAGTGATGATGACCACTTAAAAGACCTCTCATTAC
ACAAAAACCAGACAGTAGTGGACGTTGCAGTTCTCACATCTTTTCTACAGGATGAGAAAG
TGAAAGAAAGCTATGTATGAAGAATCCTGTTTATACGGGGTGGCTGAAAGTAAAGAGGAA
CTAGACTTTCTTTGCACCATGTGAAGTGTGTGGAGAAAAGAGCCAGAAGTTGATGTGG
GAAGAAGTAAACTGGATACTGTACTGATACTATTCAATGCAATGCAATTCAATGCAATGA
AAACAAAATTCATTACAGGGGCAGTGCCCTTTGTAGCCTATGTCTTGTATGGCTCTCAAG
TGAAAGACTTGAATTTAGTTTATACCTATACCTATGTGAAACTCTATTATGGAACCCAA
TGACATATGGGTTTGAACCTCACACTTTTTTTTTTTTTTTTGTTCCTGTGTATTCTCATT
GGGGTTGCAACAATAATTCATCAAGTAATCATGGCCAGCGATTATTGATCAAAATCAAAA
GGTAATGCACATCCTCATTCACTAAGCCATGCCATGCCAGGAGACTGGTTTCCCGGTGA
CACATCCATTGCTGGCAATGAGTGTGCCAGAGTTATTAGTGCCAAGTTTTTCAGAAAGTT
TGAAGCACCATGGTGTGTCATGCTCACTTTTGTGAAAGCTGCTCTGCTCAGAGTCTATCA
ACATTGAATATCAGTTGACAGAATGGTGCCATGCGTGGCTAACATCCTGCTTTGATTCCC
TCTGATAAGCTGTTCTGGTGGCAGTAACATGCAACAAAAATGTGGGTGTCTCCAGGCACG
GGAAACTTGGTTCCATTGTTATATTGTCCATGCTTCGAGCCATGGGTCTACAGGGTCAT
CCTTATGAGACTCTTAAATATACTTAGATCCTGGTAAGAGGCAAGAATCAACAGCCAAA
CTGCTGGGGCTGCAACTGCTGAAGCCAGGCATGGGATTAAAGAGATTGTGCGTTCAAAC
CTAGGGAAGCCTGTGCCCATTTGTCTGACTGTCTGCTAACATGGTACACTGCATCTCAA
GATGTTTATCTGACACAAGTGATTATTTCTGGCTTTTTGAATTAATCTAGAAAATGAAA

Fig. 9E



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Exon	Exon Forward Primer (bp)	SEQ ID No.	Reverse Primer	SEQ ID No.	intron (kb)	intron (kb)
exon 1	140 GGCTGGATTAGCAGTCTCTCA	70	ATCCCCAACTCAAAACCACA	119	intron 1	>6.413
exon 2	94 GGATTTCCAGATCCCAGTG	71	AAGTCCAATTTAGCCCACGTT	120	intron 2	>4.241
exon 3	142 GACAGACTTGGCATGAAGCA	72	CCAGCCATTCAAAATTTCTCC	121	intron 3	>1.248 (1.6)
exon 4	119 GCAGTGGAGTCACTTCTG	73	GGGTGCAGGTCAATTTCCAAT	122	intron 4	>1.512
exon 5	122 CGTTTCTCACTGTCCCAAT	74	CCCCCTCACCCACCAATACAA	123	intron 5	>1.796 (3)
exon 6	177 ACTTCAAGGACCCAGCTTCC	75	TGTCCAAGGAAAGCCCTCAC	124	intron 6	>2.726 (10)
exon 7	93 TCGGTTTCTTGTGTTAAACTCA	76	AGGACTCTTGGCCAGACTCA	125	intron 7	4.975
exon 8	241 TCCCAAGGCTTTGAGATGAC	77	AGGAGATGACACAGGCCAAG	126	intron 8	>2.311 (.5)
exon 9	140 GGCTCCAAAGCCCTTGTA	78	CGCACACTCTGAAGCTACC	127	intron 9	0.332
exon 10	117 GCTGCTGTGATGGGTATCT	79	ACCTCACTCACACCTGGGA	128	intron 10	4.208
exon 11	198 TTTGTAAATTTGTAGTGTCTCTCA	80	GCCTCTGCCTGAACCTTAT	129	intron 11	0.747
exon 12	206 TAGTCAGCCCTTGCCTCCTA	81	CAAAATCATGACACCAAGTTGAG	130	intron 12	0.523
exon 13	177 AAAGGGCTTGGTAAGGTA	82	CATGCACATGCACACACATA	131	intron 13	1.787
exon 14	223 GATGTGGTGTCTCTCTAGC	83	CCTTAGCCCGTGTGAGCTA	132	intron 14	1.747
exon 15	222 CAAGTGAGTGTGGGATTG	84	TGCTTTTATTCAGGGACTCCA	133	intron 15	1.059
exon 16	205 GCAATTCAAATTTCTCCAGG	85	CCCATGCACTGCAGAGATTTC	134	intron 16	1.105
exon 17	114 TCAAGGAGGAATGGACCTG	86	AAGGCAGGAGACATCGCTT	135	intron 17	1.789
exon 18	172 CTGAAGTTCAAGCGCAGTG	87	GGGATCAGCATGGTTTCTTA	136	intron 18	0.99
exon 19	132 TGCAGACTGAATGGAGCATC	88	GCTTAAGTCCCACTCCTCTCC	137	intron 19	1.307
exon 20	143 GCCAGGGACACTGTATTCT	89	ATTTTCTCTCCGATGTGTGT	138	intron 20	0.204
exon 21	138 AGGTCTCTGCTTCACTCA	90	TCACAGAAGCCTAGCCATGA	139	intron 21	0.706
exon 22	221 CCAGTGTCTACCCCTGCTAA	91	AACAGAGCAGGAGATGGTG	140	intron 22	>0.866 (1.7)
exon 23	73 CACACACAGAGTCTTTGGA	92	TCTGCACCTCTCTCTCTCTG	141	intron 23	0.986
exon 24	203 ACCTGGAACAGGTGTGGTGT	93	ACTGGGGCCAAACATTATCA	142	intron 24	1.668
exon 25	49 GGGCTAACATGCCACTCAGTA	94	CTTCCCATCTGCAACAAAC	143	intron 25	0.196

Fig. 10 (SHEET 1 OF 2)



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exon 26	114	GTTTGTTCAGATGGGGAAG	95	GCTAAAGGCCATCCAAAGAA	144	intron 26	326	1.396	1.4
exon 27	149	CACCAGAAGAGGAGCATGG	96	TCAAGTCATCTGGGCATAA	145	intron 27	327	1.649	1.6
exon 28	125	CTGGACTCGTAGGATTTGC	97	TCTGAAGTCCATTCCTCTGG	146	intron 28	328	>0.728(1.4)	1.4
exon 29	99	GCCTGTCCACAGAAATGCTT	98	CAATGTGGCATGCAGTTGAT	147	intron 29	329	>2.589(3)	3
exon 30	190	TTACGGAATGATCCTGTGCTC	99	GAAGCTACAGCCCATCCT	148	intron 30	330	1.521	1.5
exon 31	95	AGTCAGGTTTCCGGTCACAC	100	CAATTCCTCCACTGTTTCAG	149	intron 31	331	>0.944(\)	>0.9
exon 32	33	CCGTTCTTATATCTCAGGTG	101	CCAAGGTTTCACTGCAATCCA	150	intron 32	332	>1.062(/6.5)	>1.0
exon 33	106	CCTGTACACACTCGCACCTGA	102	GATCCGTTTAACTGCAAC	151	intron 33	333	1.475	1.5
exon 34	75	TGTTGTCCACAGGTTCAGAA	103	ATGCCCTGCCAATCTTAC	152	intron 34	334	0.522	0.5
exon 35	170	TGAGGTTTATGGGCATGGTT	104	CTCTGCAGCTGTTCCCTTAC	153	intron 35	335	1.228	1.2
exon 36	178	ATGTTTTCCTTGGCTGTGC	105	TATCAATCCATGGCCCTGAC	154	intron 36	336	>1.898(2)	2
exon 37	116	ATCTGCCCTTCTTGTCTGA	106	AGAGTCCTGCCCTCCTTCT	155	intron 37	337	0.112	0.1
exon 38	145	AGGAGCTGCACAGTGGATA	107	AAGGCAGTCAGCAGTGTCAA	156	intron 38	338	1.545	1.5
exon 39	124	TCACTCCCATATTTTCAGACTTGA	108	GGGGAACATCCTGTGCTTAG	157	intron 39	339	1.087	1.1
exon 40	130	TGTTTATGGAGATCGGTGAA	109	CCATTGGTGAGTGTTCCTT	158	intron 40	340	0.265	0.3
exon 41	121	CGTTAGAGACTGAATCTTTGTCTG	110	AGTCAGCAAACTGCTGGGTT	159	intron 41	341	>0.622(0.9)	0.9
exon 42	63	AGTCCTGCCCTCCACAGTTG	111	ATTGCTCCATCCTGGGCATAA	160	intron 42	342	0.909	0.9
exon 43	107	GGTAGTTACGTTTAGGGCA	112	TCATGGATGATTTTATGTGCTTC	161	intron 43	343	2.355	2.4
exon 44	142	CAGGAACATTAGCCAGATTG	113	GGGTGTGGAAGCCATAAG	162	intron 44	344	0.372	0.4
exon 45	135	CATGTATGTGTAGACAGCATGA	114	GCCAATCATACAACAGCCCT	163	intron 45	345	>1.059(1.3)	1.3
exon 46	104	CTGTTTCAAAGATGCTTCTGC	115	TGATCGCATATTCTACTTGGAAA	164	intron 46	346	0.483	0.5
exon 47	93	CCTAGGAAGCTGGAATGCTG	116	TCCCTTTATTTTAGAGGCACCA	165	intron 47	347	0.659	0.7
exon 48	244	GGGTTCCAGGTTTCAGTAT	117	GATCAGGAATTCAGCACCAA	166	intron 48	348	0.941	0.9
exon 49	295	CTTGACCTAATTTCAACATCTGG	118	TGGGTTCCATAATAGAGTTTCACA	167	intron 49	349	>1.075	

Fig. 10 (SHEET 2 OF 2)



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ERRORS IN PUBLIC SEQUENCE (differences between samples and Genbank entry AJ012376.1):				
Exon/Intron	Nucleotides	Amino Acid Change	Sequence difference/context	SEQ ID NO:
2	T150C A152G	no change	Public sequence: TGTCAGCTGTACTCTGGAAGTGG	168
			Correct sequence: TGTCAGCTGCTGCTGGAAGTGG	169
7	C839T	no change	Public sequence: AGGAGCTGGCCGAAGCCACAA	170
			Correct sequence: AGGAGCTGGCTGAAGCCACAA	171
33	C4738T	T1495I	Public sequence: AATGATGCCACCAACAATG	172
			Correct sequence: AATGATGCCATCAACAATG	173
35	C5017T	P1588L	Public sequence: GAGTGGCTCCGATGACCACA	174
			Correct sequence: GAGTGGCTCTGATGACCACA	175
43	G5995A	R1914K	Public sequence: TTCCTTAACAGAAATAGTATC	176
			Correct sequence: TTCCTTAACAAAAATAGTATC	177
48	C6577T	P2108L	Public sequence: GGAAGTGTCCAAAAGAGAAA	178
			Correct sequence: GGAAGTGTCTTAAAAGAGAAA	179
49	G6899A	not applicable	Public sequence: AGTAAAGAGGGACTAGACTTT	180
			Correct sequence: AGTAAAGAGGAAC TAGACTTT	181
Mutations:				SEQ ID NO:
13	A1864G	Q597R	More common: GCCTACTTGCAGGATGTGGTG	182
			Less common: GCCTACTTGGGGATGTGGTG	183
14	delta CTT 2151-3	delta L093	More common: CCTCATTCCTCTTCTTGTGAGCG	184
			Less common: CCTCATTCCT/CTTGTGAGCG	185
15	G2385A	V771M	More common: GCAGGACTACGTGGGCTTCAC	186
			Less common: GCAGGACTACATGGGCTTCAC	187
18	C2799T	R909Stop	More common: AAAAGTCTACCGAGATGGGAT	188
			Less common: AAAAGTCTACTGAGATGGGAT	189
18	C2860T	T929I	More common: GGCCAGATCACCTCTCTTCTG	190
			Less common: GGCCAGATCATCTCTTCTG	191
22	T3346C	M1091T	More common: ACACACCAATGGATGAAGCG	192
			Less common: ACACACCAACGGATGAAGCG	193

Fig. 11 (SHEET 1 OF 4)



Serial No.: 09/526,193
 Applicant: Hayden et al
 Filed: 15 March 2000
 Attorney Docket: 760050-19

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Intron 24	(+1) G to C splice donor site	Altered transcript length	More common: Less common:	CCTGGAAGAGTAAGTTAAGT CCTGGAAGAGTAAGTTAAGT	194 195
30	T4503C	C1477R	More common: Less common:	GCTGCCCTGTGTGTCCTCCAGG GCTGCCCTGTGTGTCCTCCAGG	196 197
35	GG 4958-57 to C	frameshift at aa 1628	More common: Less common:	TAGCCATTATGGAATTACTGCT TAGCCATTATCAATTACTGCT	198 199
41	delta AAGATG 5752-7	delta(E,D)1893-1894	More common: Less common:	GATGAAGATGAAGATGTGAGCGGGGA GATGAAGATG/TGAGCGGGGA	200 201
48	C6504T	R2144Stop	More common: Less common:	AATAGTTGTACGAATAGCAGG AATAGTTGTATGAATAGCAGG	202 203
Promoter Variants: Location	Position Relative to Xenon cDNA	Position Relative to SEQ ID NO: 14 Containing Exon 1			SEQ ID NO:
1	G57C	8216	More common: Less common:	ACACGCTGGGGTGTGCTGGCTG ACACGCTGGGGTGTGCTGGCTG	204 205
5	(-)4 ins. G	8158	More common: Less common:	GACCAAGCACGGCTCCCTG GACCAAGCACGGCTCCCTG	206 207
5	A (-)380 G	7780	More common: Less common:	CATTTTCTTAGAAAAGAGAGGT CATTTTCTTAGAAAAGAGAGGT	208 209
5	A (-)479 C	7681	More common: Less common:	GAAAATTAGTATGTAAAGGAAG GAAAATTAGTCTGTAAAGGAAG	210 211
5	A (-)738 G	7422	More common: Less common:	CCTCCGCTGCCAGGTTACGGATT CCTCCGCTGCCAGGTTACGGATT	212 213
5	A (-)1045 G	7115	More common: Less common:	TATGTGCTGACCATGGGAGCTTGT TATGTGCTGACCATGGGAGCTTGT	214 215
5	A (-)1113 G	7047	More common: Less common:	GTGACACCAACGGAGTAGGG GTGACACCGAGCGGAGTAGGG	216 217
5	(-)1181 ins. CCT	6979	More common: Less common:	AGTATCCCT/TGTTACAGAGAA AGTATCCCTCCCTTGTTCACAGAA	218 219

Fig. 11 (SHEET 2 OF 4)



Polymorphisms:					
Exon/Intron	Nucleotides	Amino Acid Change		Sequence difference/context	SEQ ID NO:
5	G548A	no change	More common:	CTGGGTTCCTGTATCACAACC	220
			Less common:	CTGGGTTCCTATATCACAACC	221
6	G730A	R219K	More common:	GGCCTACCAAGGGAGAAACTG	222
			Less common:	GGCCTACCAAGGAGAAACTG	223
Intron 7	G(+)/2383 T	Not applicable	Allele 1:	TTTAAAGGGGGTGTATTAGGA	224
			Allele 2:	TTTAAAGGGGGTGTATTAGGA	225
Intron 7	G(+)/3035 T	Not applicable	Allele 1:	GAAGAAATTTGTTTTTTGATT	226
			Allele 2:	GAAGAAATTTTTTTTTTGATT	227
8	C1010T	no change	More common:	GCGGGCATCCCGAGGGAGGGG	228
			Less common:	GCGGGCATCCTGAGGGAGGGG	229
8	G1022A	no change	More common:	AGGGAGGGGGGCTGAAGATCA	230
			Less common:	AGGGAGGGGGACTGAAGATCA	231
Intron 9	(-)/42 ins. G	Not applicable	More common:	AGGAGCCAAACGCTCATTTGT	232
			Less common:	AGGAGCCAAAGCGCTCATTTGT	233
Intron 13	T(+)/24 A	Not applicable	More common:	AAGCCACTGTTTTTTAACCACT	234
			Less common:	AAGCCACTGTATTTTAACCACT	235
15	A2394C	T774P	More common:	CGTGGGCTTCACACTCAAGAT	236
			Less common:	CGTGGGCTTCCCACTCAAGAT	237
15	G2402C	K776N	More common:	TCACACTCAAGATCTTCGCTG	238
			Less common:	TCACACTCAACATCTTCGCTG	239
Intron 14	C(+)/16 T	Not applicable	Allele 1:	GCAGCCTCACCCGCTCTTCCC	240
			Allele 2:	GCAGCCTCACTCGCTCTTCCC	241
17	A2723G	I883M	Allele 1:	AGAAGAGAATATCAGAAATCT	242
			Allele 2:	AGAAGAGAATGTCAGAAATCT	243
Intron 17	C(+)/2000 G	Not applicable	Allele 1:	GCGCAGTGCCTGTGTCTTTA	244
			Allele 2:	GCGCAGTGCCTGTGTCTTTA	245

Fig. 11 (SHEET 3 OF 4)



21	T3233G	no change	More common: Less common:	GATCTAAGGTTGTCATCTCTGG GATCTAAGGTTGTCATCTCTGG	246 247
Intron 21	G(+118 T	Not applicable	Allele 1: Allele 2:	CTCTCTCTCTTAGGACAGAAGAGA CTCTCTCTCTTAGGACAGAAGAGA	248 249
Intron 21	A(+1563 G	Not applicable	Allele 1: Allele 2:	CATTCTAGGGATCATAGCCAT CATTCTAGGGATCATAGCCAT	250 251
Intron 24	G(+1321 T	Not applicable	Allele 1: Allele 2:	AAGTACAGTGGGAGGAACAGCG AAGTACAGTGGGAGGAACAGCG	252 253
Intron 29	A(-1624 G	Not applicable	Allele 1: Allele 2:	AATTCTTAAAAATAGAAATGCA AATTCTTAAAAATAGAAATGCA	254 255
Intron 31	T(+130 C	Not applicable	More common: Less common:	GGCCCCCTGCTTATTTATTA GGCCCCCTGCTTATTTATTA	256 257
Intron 33	A(+1732 G	Not applicable	Allele 1: Allele 2:	TGAGAGAAATTAATGACCCCG TGAGAGAAATTAATGACCCCG	258 259
Intron 33	C(+1898 T	Not applicable	Allele 1: Allele 2:	TTTGCTGAACAATCACTGCA TTTGCTGAACAATCACTGCA	260 261
Intron 34	C(+1234 T	Not applicable	Allele 1: Allele 2:	AACCTCAGTTCCTCACTGCTG AACCTCAGTTCCTCACTGCTG	262 263
34	G4834A	R158TK	More common: Less common:	CTGGACACCAAGAAATATGTC CTGGACACCAAGAAATATGTC	264 265
37	C 5266G	S1731C	More common: Less common:	TCCTATGTCCTCCACCAAT TCCTATGTCCTCCACCAAT	266 267
Intron 43	T(+118 C	Not applicable	More common: Less common:	AAGAAGTGGCTGTATTTTTC AAGAAGTGGCTGTATTTTTC	268 269
Intron 43	C(+1665 G	Not applicable	Allele 1: Allele 2:	AACTGATTTGATTTGGTATAGCTG AACTGATTTGATTTGGTATAGCTG	270 271
48	C6521T	no change	More common: Less common:	CAGGGTCCAAACCCGACCTGA CAGGGTCCAAACCCGACCTGA	272 273
Intron 10	(+114 ins. T	Not applicable	More common: Less common:	GGTCAGGGATGGGGACAG GGTCAGGGATGGGGACAG	284 285
Exon 16	G2547A	V8251	More common: Less common:	CCACTTCGGTCTCCCATG CCACTTCGATCTCCCATG	286 287
Polymorphism in an ABC1 BAC contig: This polymorphism is within approximately 200Kb of the ABC1 gene					SEQ ID NO:
	A or G	Not applicable	Allele 1: Allele 2:	TTGGGAGGCTAAGGCAGGAGAA TTGGGAGGCTAAGGCAGGAGAA	274 275

Fig. 11 (SHEET 4 OF 4)



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Genomic contig containing ABC1 exon 1:

Underline = putative promotor element

acctcttatagaatgatagaattcctctggaatgattggataacttcatttcaccttgacttttaccttgaggattt
cttacccttttggcttctcaaatttgactattaaaatgttgctttaaaaataggaacacagtttcaggggggagtac
cagcccatgacccttctgcaaggccccctaactcaaggtagtttccctggaactgtggtttatggaatgtttcaggagt
gtgaggaggatataatttaaggctgtcctagcaaggatacccttaaggatagagggcccagtagcatctggaggccagaa
aagttaaactgaggcagtcagattagcttcaggctcaattaagctgatgggtcagcctgggagaaattgcaggatgact
ctcaatatccctcccacccccacagcagccacgatctgtctgtctttaatcatgggtgcagtgaacctgttctttcca
gggtgtcttggccttcagtaaccttgttaggctgtcctgaacgtgggtaccgatccaaagacacatgatcagagaggc
aattagagaacagaccttttccaaagcaagcatgttctgttgggttagaagtttcatgtcctaattattataggacct
gtgcatctctctggagatgaggcacatgatctgtgattcttggcttttgtgtcaacatctcatgaataggcaat
cagagctttggcaccatgtattttcagttccatatctgatgtagttaaattccacctcctgtcttgtagtactggcaa
gctgtttttgatataagacatctagaacactgtaaatataaacatttttatttgtctattatacctcaattacgaaaa
agacatctagaagcaacctcatcaagagagatactgaggccgggcatggtagctcacacttgcaatcccattactttgg
gaggctgaggcaggtagatcacttgagggtcaagagtttgaaaccagcctggccaacatgttgaaacctgtctctatta
aaaatacaaaaaagttagctgggcttgggtgggtgggcacctgtaatcccagctactccggaggctgaggcaggagaatca
cttgaacctgggaggcagaggttgcagtgagctgagatcacaccactgcactccaacctgggcaccagagttagattac
atctaaaaataaaaaaagtaataaaaaagagagatatgtatagctgttgggtgaaatttcaacttccatctcacttc
tggttaacttttggagtttgttgaacaaagtgaatacacgcacatacacacacacatactctcttgttgttttaa
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Fig. 12 (SHEET 1 OF 32)

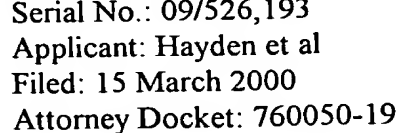


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Fig. 12 (SHEET 3 OF 32)



SEQ ID NO: 15

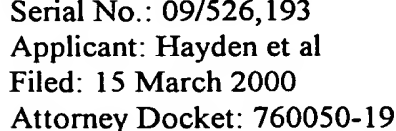
[illegible]

Fig. 12 (SHEET 4 OF 32)



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Fig. 12 (SHEET 5 of 32)



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SEQ ID NO 16

Genomic contig containing ABC1 exon 3:

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Fig. 12 (SHEET 6 OF 32)



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Fig. 12 (SHEET 7 OF 32)

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SEQ ID NO 17

Genomic contig containing ABC1 exon 4:

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Fig. 12 (SHEET 8 OF 32)



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SEQ ID NO 18

Genomic contig containing ABC1 exon 5:

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SEQ ID NO 19

Genomic contig containing ABC1 exon 6:

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Fig. 12 (SHEET 10 OF 32)



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SEQ ID NO 20

Genomic contig containing ABC1 exon 8:

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Fig. 12 (SHEET 11 OF 32)



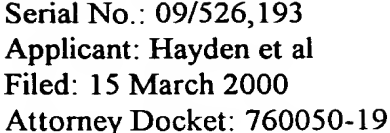
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Fig. 12 (SHEET 12 OF 32)



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Fig. 12 (SHEET 13 OF 32)



SEQ ID NO 21

Genomic contig containing ABC1 exon 9 through 22:

Fig. 12 (SHEET 14 OF 32)



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Fig. 12 (SHEET 15 OF 32)

Fig. 12 (SHEET 16 OF 32)



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TTTTGGGTTTGGCTGTGAGTACTTTGCCCTTTTTGAGGAGCAGGGCATTGGAGTGAGTGGGACAACCTGTTTGAGAGTC
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aatcattaccagatccctaactctcttggctcttaactgcagacagagatgtccacagctcatcaaaggctctgctt
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SEQ ID NO: 22

Genomic contig containing ABC1 exon 23 to 28:

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GATGGTACCTTGCCAGCAAGACGAAACAGGCGGGCCTTCGGGGACAAGCAGAGCTGTCCTTCGCCCCGTTCACTGAAGATGA
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acacggtggaat

Fig. 12 (SHEET 21 OF 32)

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SEQ ID NO: 23

Genomic contig containing ABC1 exon 29:

[illegible]

Fig. 12 (SHEET 22 OF 32)



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SEQ ID NO: 24

Genomic contig containing ABC1 exon 30 and 31:

tcttgccagtctctactcatttttcagcacatcgagcataagatccagactctttccaggcctctctcatctggctcct
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gaaatgcatttcttccctagggcctttgtacctgcacttgccatcgcttttgctcagaatgttcttttgccaagcttttg
cccagcttggttctccatcattgttatgttttggtgaaatgtcttctcttagtaggttcatttctccccagtcactgtctt
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CAGGGGAGGAAGAGTGGACCACTGCCCGAGTTCGCCAGACCATCATGGACCTCTTCCAGAAATGGGAACCTGGACAATGCAG
AACCTTCACCTGCATGCCAGTGTAGCAGCGACAAAATCAAGAAGATGCTGCCGTGTGTCCCCCAGGGGCAGGGGGCT
GCCTCTCCACAgtgagtcactttcagggggtgattgggcagaaggggtgcaggatgggctggttagcttccgcttgga
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cactgtactccagcctgagcaacacagcaaaactccatatcaaaaaataaaatgaataaaataacagctaattctagtc
cagtataactccagtgaacagaagatttattaggcatagtgaatgatggtgcttctctaaaaatctcttgactacaaagaa
tctcatttcaatgtttattgttttagatgttcagaataaattcttgggaaagaccttggcttgggtgtaagtgaattaccag
tgccgagggcagggtgaaccaagctcagtgctggttgactgagggcagtgctggtgacctgtagtcagggtttccggtca
cactgtggacatggtcactgttgccttgatttgttttctgtttcaattcttgtctataaagaccgctatgcttgggttt
catgtgatgacagAGAAAACAAAACACTGCAGATATCCTTCAGGACCTGACAGGAAGAAACATTTCCGATTATCTGGTGA
AGACGTATGTGCAGATCATAGCCAAAAGgtgacttttactaaacttggccctgccttattattactaattagaggaat
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tattatcccaaactagaaaagatgacgagagggactgtgaacattcagttgtcagcttcaaggctgaggcagcctggtct
agaatgaaaatagaaatggattcaacgtcaaattttgccac

Fig. 12 (SHEET 23 OF 32)



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SEQ ID NO: 25
Genomic contig containing ABC1 exon 32: _

gcatgctggagtgatagtgaccatgagtttctaagaaagaagcataatttctccatgtcatccacaattgaaatatta
ttgttaattgaaaaagcttctaggccaggcacggtggctcatgcctgtaatcccagcactttaggagccaaggcgggtgg
atcacttgaggtcaggagtttgagaccagcctggccaacatgggaaaccctgtctctactaaaaatacaaaataagctg
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ttggggattgtttgtcactcacacacttgtgggtgccatctcactgtgagga

Fig. 12 (SHEET 24 OF 32)



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SEQ ID NO: 26

Genomic contig containing ABC1 exon 33 to 36:

gctttatagagtttctgcctagagcatcatggctcagtgcccagcagccccctccagaggcctctgaatatttgatatact
gatttccttgaggagaatcagaaatctcctgcagggtgtctagggatttcaagtaagtagtggtgtgaggggaatacctac
ttgtactttcccccaaaccagattcccagggcttcttaaggactcaaggacaatttctagggcatttagcacgggactaa
aaaggtcttagaggaaataagaagcgccaaaaccatctctttgactgtatttcaaccatttgccttctgggttttga
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cgtcagggggccgaaggctccttggtactgatttccgtcttttctctctgccttttccccaaagggccaggacccctgga
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tctgaggcaaaatttagccctcctttgaacaggaatttgactcagtgaaacctgtacacactcgactgagctgtgtgt
gatgatactgtgcacccactgtctgggttttaagtgcaggctgttcttttagGTATGGCGGCTTTTCCCTGGGTGTCAG
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AGGACTGGACACCAGAAATAATGTCAAGgtaaaccgtgtcttctgttagtagctttttgatgaacaataatccttatg
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aatgagttaaagggtataaggctcctcaccacagcgcctgcccacatagtcagtgatcactatgtcctgaacactgtaatta
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tgggtatgcacctgcctgcaggagcccggtttgggggcatccttgtaacctggatgttttcttccagGTGTGGTTCAA
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AGAACCCTAGCCATTATGGAATTACTGCTTTCAATCATCCCCCTGAATCTCACCAAGCAGCAGCTCTCAGAGGTGGCTCTg
taagtgtggctgtgtctgtatagatggagtggggcaaggagaggggttatggagaaggggagaaaaatgtgaatctcatt
gtaggggaacagctgcagagaccgttatattatgataaatctggattgatccaggctctgggcagaagtataagtttac
gaattggctgggttgggcttcttgaactgcagaagagaaaaatgacactgatatgtaaaaatcgtaaacatttagtgtaattca

Fig. 12 (SHEET 25 OF 32)



tataaagtgaagttcaaaaattgttaattaaattataaatttaattataaagtgtttaatcagtttgatttgtttaaaaacca
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gtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgaagtttaagccaggatgagctagtttaagtatgcagcctttggagtc
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gcccagcactcagcacagagttgatatttcacacacattagataacctttcctgtatgtggagcatggcagttcctgtttc
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TGAAGCCTGTCTACTTGGCTCTCTAATTTTGTCTGGGATATGgtaaggacacaggcctgctgtatctttctgatgtct
gtcagggccatggattgatatggataagaaagaaagagctctggctatcatcaggaaatgttccagctactctaaagatg
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agatctttgctgtttataccaagccccctagactgtgtcactcttctgatccggttgctccttgatggccatgctgtata
ttgtgaatgtcccgttttcaaaagcaaagccaagaattaaccttggtgttcaggctgtggtctgaatgggttatgggtccag
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aacttagtggttaaccaaaccctccatttcacacaaatgattgtgaaattcgggtctccttcattctatacaaatcatt
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agtccttgaaacctctctgtcttctgggtattatctgtcctcctgcttttagagctcctgaaatttgctagaagca
tgtcttcatctaagttgttgataaacacatcaagtaggattggactgaggcagagccctgtagtctgaagctgcagttct
tctagcggctgacaagccccactatcacttccctgctggtgctttgtctgccagctgtgaattctcataattgtcctat
cgtcaagtcctttatttctgcattttactgcttgatacactgtcaggacagactttaaaattatttctcagtgcgatgaaac
aattctgacattcatgttatgagcagttacctcataaatagattacatg

Fig. 12 (SHEET 26 OF 32)



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SEQ ID NO: 27

Genomic contig containing ABC1 exon 37 to 41:

aaattactctgactgggaatccatcggttcagtaagtttactgagtgtagacaccttggcttgactggttgaaagacagaaa
gggcatgtagtttataaaatcagccaaggggaaaatgcttgtcaaaatgtattgtcgggtattttgattaatagtttatg
tggcttcattaattcagagttactctccaatatgtttatctgccctttcttgtctgataatggtgaaaacttgtgtgatg
cattgtatatttgatttaggggtgaactggatgtctttgttttcaacttttagTGCAATTACGTTGTCCCTGCCACACTGG
TCATTATCATCTTCATCTGCTTCCAGCAGAACTCCTATGTGTCTCCACCAATCTGCCTGTGCTAGCCCTTCTACTTTTG
CTGTATGGGtaagtcacctctgagtgagggagctgcacagtggataaaggcatttgggtgcccagtgtcagaaggaggggcag
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TCAAGATCCCCAGCACAGCCTATGTGGTGCTCACCAGCGTGAACCTCTTCATTGGCATTAAATGGCAGCGTGGCCACCTTT
GTGCTGGAGCTGTTACCGACAATgtgagtcagtcagagagaacactcctgctgggatgagcatctctgggagccagagg
acagtggttaattgtgatcttattccacttgtcagtggtattgacactgctgactgccttgtcctgtcttcagagtcctgt
cttccctgagaaggcaagcacctttctttcttgcctgtgccttacattttgctgggtcaagcctttcagtttcttttgaca
gttttttttacttctttcttttttcaatgttgccttaccagagtagctcctctgccttccactttacacatgagagct
gggagcagcattcagtcctaaggcttttaccatcacctctcttgggtgtttttattgtcatctctaagatcaatgccttta
gccttgatcataaccttgaactctaattctcaaatctcacttgcctagtggtattgtccatttagatagtatatagatac
cccaacctggatagtgcctagttttctttcccttggaaacttaatgcttttcttggcatccctgtcacactcagtgggcac
taccatccactcggttggccaagctggctcttagagttatcctagatgcttgccttgcctgttgagatttcccacattca
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tctgaaattctgattgatactgggtcataaaaagttttcccaaactcagacttggaaagtgatcactctcttgttactctt
ttttccttgtcatgggtgatagccatttgtgtttattggaagatcggtgaattttaaggacataggcccaatttgagg
aaggggccatgggtttttgatccctccattctgaccggatctctgcattgtgtctactagGGGAGAATCGCTTTGTGTACCC
ATTATCTTGGGACTTGGTGGGACGAAACCTCTTCGCCATGGCCGTGGAAGGGGTGGTGTCTTCTCATTACTGTTCTGA

Fig. 12 (SHEET 27 OF)



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TCCAGTACAGATTCTTCATCAGGCCAGgtgagctttttcttagaaccogtggagcacctgggtgaggggtcacagaggag
gcgcacagggaaacactcaccaatgggggttgcaatgaactgaactcaaaatatgtgataaaactgattttcctgatgtg
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tatatgcttacatttatgtgttagttattaaaacataactaatattgtatatctagtcaaactgagtagagagataatggt
gatt

Fig. 12 (SHEET 28 OF 32)



SEQ ID NO: 28

Genomic contig containing ABC1 exon 42 to 45:

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agagccagggaggtgcaaggactggggagggtagaggcaggaaccctgcctgccaggaagagctagcatcctgggggcag
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Fig. 12 (SHEET 30 OF 32)



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SEQ ID NO: 29

Genomic contig containing ABC1 exon 46 to 49:

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tccccaaaaacctattattgagaatttaattacataaaaaagttactcagaatatttgagtttctctgcatcaataagacat
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agttaaaatttaagctgtttcaaagatgcttctgcatttaaaaaacaaatttatctttgattttttttccccccagcaaat
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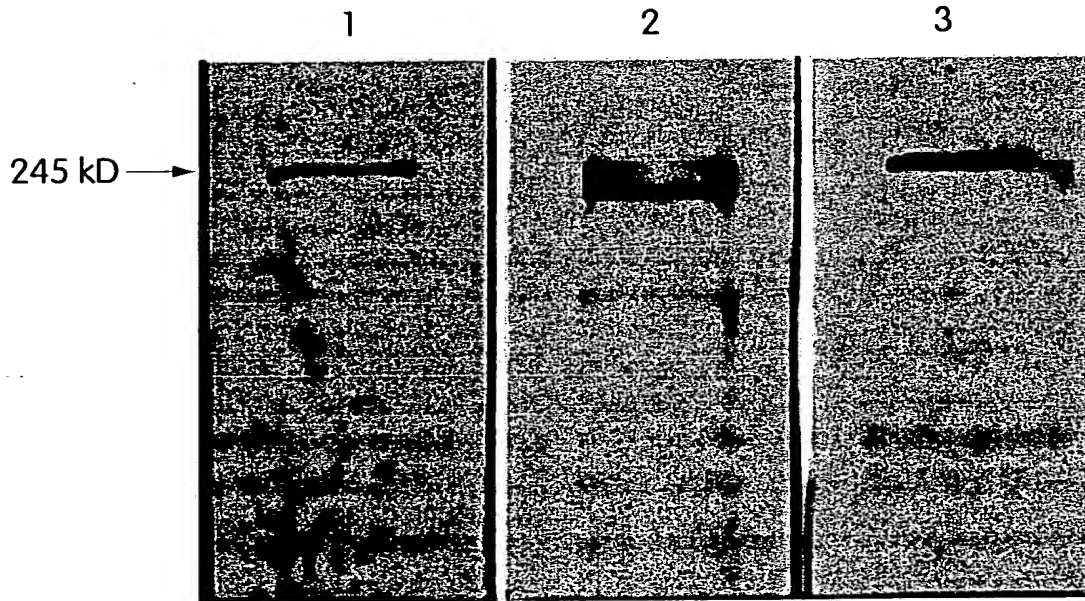


Fig. 13

Control

[illegible]

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Serial No.: 09/526,193
Applicant: Hayden et al
Filed: 15 March 2000
Attorney Docket: 760050-19

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TECH CENTER 1600/2900

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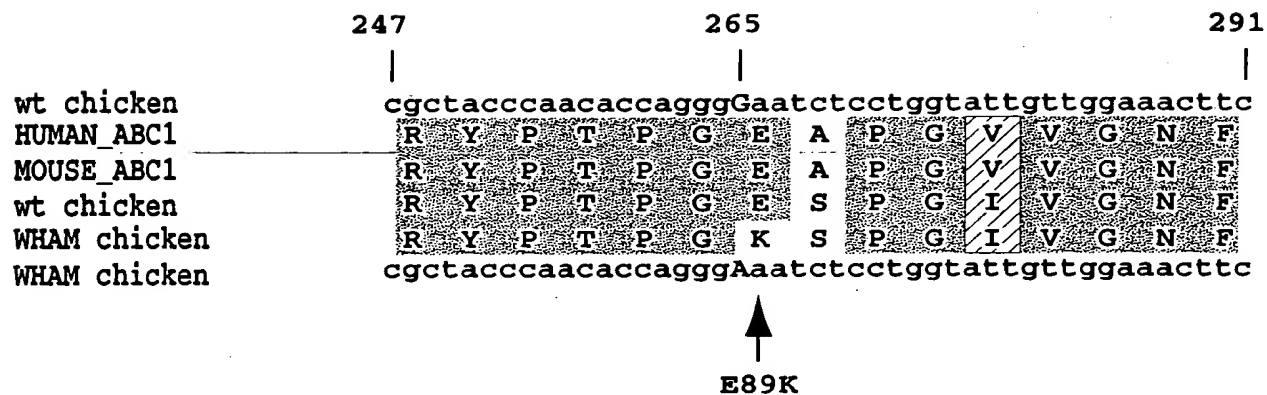


Fig. 15



SEP 18 2002

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TECH CENTER 1600/2900

No. Name	Location in SEQ ID No. 14	Sequence	Sequence Strand Length
1 PPPE	58-69	AGGTAAAGTCA	12 Complement
2 PPPE	1997-2009	AGAGTAGAGGCA	13 Lead
3 PPPE	2150-2161	ATGTCAAGTTCA	12 Lead
4 PPPE	2156-2169	AGTTCAAAAGGCCA	14 Lead
5 PPPE	4126-1139	AGGCCAGCAGGGCC	14 Complement
6 PPPE	5075-5087	AGGGCAGAAGTGA	13 Lead
7 PPPE	6604-6615	ATGCCAAGGTCA	12 Complement
8 PPPE	6731-6743	GGGGCAAGGGTA	13 Complement
9 PPPE	7220-7233	AGGTAATGAGGACA	14 Complement
10 PPPE	7554-7568	GGATCAGGAGGTCA	15 Complement
1 SRE	159-166	CAGCCCAT	8 Lead
2 SRE	1133-1140	CAGCTCAC	8 Complement
3 SRE	1145-1152	CACACCCAC	8 Lead
4 SRE	1809-1816	CAGCCCTC	8 Complement
5 SRE	1894-1901	CAGCCCAT	8 Lead
6 SRE	2563-2570	CAACCCAC	8 Lead
7 SRE	3303-3310	CAGCTCAC	8 Lead
8 SRE	3470-3477	CCGCCAC	8 Lead
9 SRE	4784-4791	CTCCCCAC	8 Complement
10 SRE	4802-4809	CAGCCTAC	8 Complement
11 SRE	4970-4977	CACCTCAC	8 Complement
12 SRE	6487-6494	CAGCCTAC	8 Complement
13 SRE	6565-6572	CACCCAAC	8 Complement
14 SRE	6727-6734	CACCCCTCA	8 Lead
15 SRE	7041-7048	CACCCAAC	8 Lead
16 SRE	8059-8066	CAGCCCTC	8 Complement
1 ROR (retinoic acid receptor related)	166-172	AGGGTCA	7 Complement
2 ROR (retinoic acid receptor related)	166-173	AAGGGTCA	8 Complement
3 ROR (retinoic acid receptor related)	263-370	ATGGGTCA	8 Lead
4 ROR (retinoic acid receptor related)	264-370	TGGGTCA	7 Lead
5 ROR (retinoic acid receptor related)	2218-2225	TAGGGTCA	8 Lead
6 ROR (retinoic acid receptor related)	2219-2225	AGGGTCA	8 Lead
7 ROR (retinoic acid receptor related)	3643-2649	TGGGTCA	7 Lead
8 ROR (retinoic acid receptor related)	6604-6610	AAGGTCA	7 Complement
1 SREBP-1 or "E box"	473-479	ACACCTG	7 Complement
2 SREBP-1 or "E box"	536-541	ACACATG	7 Lead
3 SREBP-1 or "E box"	537-543	TCATGTG	7 Complement
4 SREBP-1 or "E box"	655-661	TCATGTG	7 Complement
5 SREBP-1 or "E box"	925-931	ACACTTG	7 Lead
6 SREBP-1 or "E box"	967-973	TCACTTG	7 Lead
7 SREBP-1 or "E box"	968-974	TCAAGTG	7 Complement
8 SREBP-1 or "E box"	1053-1069	ACAGGTG	7 Complement
9 SREBP-1 or "E box"	1104-1110	TCAGGTG	7 Lead
10 SREBP-1 or "E box"	1105-1111	TCAAGTG	7 Complement
11 SREBP-1 or "E box"	1561-1567	TCACTTG	7 Lead

Fig. 16 (SHEET 1 OF 2)



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12	SREBP-1 or "E box"	1670-1676	TCAAATG	7	Lead
13	SREBP-1 or "E box"	1748-1754	ACACTG	7	Lead
14	SREBP-1 or "E box"	1749-1755	ACAAATG	7	Complement
15	SREBP-1 or "E box"	1852-1858	TCATGTG	7	Lead
16	SREBP-1 or "E box"	1853-1859	ACACATG	7	Complement
17	SREBP-1 or "E box"	1899-1905	ACAAATG	7	Complement
18	SREBP-1 or "E box"	2199-2205	ACACGTG	7	Lead
19	SREBP-1 or "E box"	2393-2399	ACAGCTG	7	Complement
20	SREBP-1 or "E box"	2669-27005	ACACCTG	7	Lead
21	SREBP-1 or "E box"	2677-2683	TCACATG	7	Complement
22	SREBP-1 or "E box"	2740-2746	ACAACTG	7	Complement
23	SREBP-1 or "E box"	2969-2975	ACAAATG	7	Lead
24	SREBP-1 or "E box"	2979-2985	ACACATG	7	Lead
25	SREBP-1 or "E box"	2981-2987	ACATGTG	7	Lead
26	SREBP-1 or "E box"	2980-2986	ACATGTG	7	Complement
27	SREBP-1 or "E box"	2982-2988	ACACATG	7	Complement
28	SREBP-1 or "E box"	3461-3467	TCAGGTG	7	Lead
29	SREBP-1 or "E box"	3462-2468	TCACCTG	7	Complement
30	SREBP-1 or "E box"	3547-3553	TCAACTG	7	Complement
31	SREBP-1 or "E box"	3752-3758	ACACATG	7	Lead
32	SREBP-1 or "E box"	4226-4232	TCACCTG	7	Lead
33	SREBP-1 or "E box"	4582-4588	ACACGTG	7	Complement
34	SREBP-1 or "E box"	4588-4594	TCAGTTG	7	Lead
35	SREBP-1 or "E box"	4861-4867	TCAGGTG	7	Lead
36	SREBP-1 or "E box"	4951-4957	ACAAATG	7	Lead
37	SREBP-1 or "E box"	5096-5102	TCAAATG	7	Complement
38	SREBP-1 or "E box"	5912-5918	ACAGTTG	7	Lead
39	SREBP-1 or "E box"	5913-5919	TCAACTG	7	Complement
40	SREBP-1 or "E box"	6245-6251	ACACATG	7	Complement
41	SREBP-1 or "E box"	6288-6294	ACAACTG	7	Complement
42	SREBP-1 or "E box"	6623-6629	TCATTTG	7	Lead
43	SREBP-1 or "E box"	6836-6842	TCACCTG	7	Lead
44	SREBP-1 or "E box"	6837-6843	ACAGGTG	7	Complement
45	SREBP-1 or "E box"	7032-7038	ACAGGTG	7	Complement
46	SREBP-1 or "E box"	7069-7075	TCAGGTG	7	Lead
47	SREBP-1 or "E box"	7101-7107	ACATATG	7	Complement
48	SREBP-1 or "E box"	7138-7144	ACAGTTG	7	Lead
49	SREBP-1 or "E box"	7139-7145	TCAACTG	7	Complement
50	SREBP-1 or "E box"	7240-7246	ACACCTG	7	Complement
51	SREBP-1 or "E box"	7467-7473	ACAGGTG	7	Lead
52	SREBP-1 or "E box"	7640-7646	TCATTTG	7	Lead
53	SREBP-1 or "E box"	7641-7647	TCAAATG	7	Complement
54	SREBP-1 or "E box"	7653-7659	TCAGTTG	7	Lead
55	SREBP-1 or "E box"	7654-7660	ACAACTG	7	Complement
56	SREBP-1 or "E box"	7735-7741	ACAAATG	7	Lead
57	SREBP-1 or "E box"	7838-7844	TCAGGTG	7	Complement
58	SREBP-1 or "E box"	7880-7886	TCATCTG	7	Complement
59	SREBP-1 or "E box"	8051-8057	TCAGCTG	7	Lead
60	SREBP-1 or "E box"	8052-8058	TCAGCTG	7	Complement

Fig. 16 (SHEET 2 OF 2)